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100.0%; Score 75; DB 14; Length 375;
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APPLICANT: Dixon, Alistair
APPLICANT: Dixon, Alistair
APPLICANT: Brooksbank, Robert
APPLICANT: Brooksbank, Robert
TITLE OF INVENITION: Identification and Use of Molecules Implicated in Pain
FILE REFERENCE: WL-A-018201
CURRENT APPLICATION NUMBER: US/10/205,194
CURRENT FILING DATE: 5200-07-24
PRIOR APPLICATION NUMBER: GB 0118354.0
NUMBER OF SEQ ID NOS: 177
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 93
LENGTH: 275
                                                                                                                                         Gaps
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                                                                                       Query Match 100.0%; Score 75; DB 16; Length 371; Best Local Similarity 100.0%; Pred. No. 0.00018; Matches 15; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
100.0%; Score 75; DB 14; Length 375;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Cytoplasmic gamma isoform of actin US-10-205-194-93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Thompson, Larry
APPLICANT: Wang, Reng
APPLICANT: Wang, Reng
APPLICANT: Greis, Kenneth
TITLE OF INVENTION: Anglogenesis Modulating Proteins
FILE REFERENCE: 865M
CURRENT APPLICATION UNDER: US/10/316,253
CURRENT APPLICATION UNDER: US/10/316,253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURKENT FILING DATE: 2002-12-10

PRIOR APPLICATION NUMBER: US 60/355,295

PRIOR FILING DATE: 2002-02-08

NUMBER OF SEQ ID NOS: 308

SEQ ID NO 88

TENGTH: 375

TYPE: PRT

ORGANISM: Rattus norvegicus
US-10-316-253-88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 88, Application US/10316253
Publication No. US20030162706A1
GENERAL INFORMATION:
APPLICANT: The Procter & Gamble Company
APPLICANT: Peters, Kevin
                                                                                                                                                                                                                                                                                            RESULT 14
US-10-205-194-93
Sequence 93, Application US/10205194
Publication No. US20030134301A1
GENERAL INFORMATION:
APPLICANT: Warner-Lambert Company
                                                                                                                                                                                                                       191 KILTERGYSFTTTAE 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 KILTERGYSFITTAE 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Rattus rattus
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-322-281-68
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Gaps
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0
              Indels
Pred. No. 0.00018;
; Mismatches 0;
Best Local Similarity 100.0%;
Matches 15; Conservative C
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1 KILTERGYSFTTTAE 15

191 KILTERGYSFTTTAE 205

Search completed: April 8, 2005, 12:51:01 Job time: 43.6667 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

- protein search, using sw model OM protein April 8, 2005, 09:58:56; Search time 9.33333 Seconds (without alignments) 154.634 Million cell updates/sec Run on:

US-09-423-351C-9 76 1 DEAQSKRGILTLKYP 15 Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: pirl: * 2: pir2: * 3: pir3: * 4: pir4: * PIR 79:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		æ				
Result No.	Score	Query Match	Length	DB	ID	Description
	76	100.0		2	C43616	actin beta, cytoso
7	91	100.0	137	7	A28258	2C -
٣	92	100.0		7	I49465	alpha-cardiac acti
4	92	100.0		~	S20097	
5	16	100.0		~	A61043	actin CA15 - sea s
9	9/	100.0		~	A03000	actin 3 - fruit fl
7	94	100.0	325	~	JC2008	m
ω	9/	100.0		8	S11452	
σ	16	100.0		~	S05430	д
10	16	100.0	349	~	B25819	actin, fetal skele
11	16	100.0	361	~	868089	
12	16	100.0		~	A26559	ţ
13	16	100.0		~	268090	actin 8 - Arabidop
14	16	100.0		~	A37431	actin, type 1 - Em
15	9/	100.0		~	A29664	- sea r
16	16	100.0		Н	ATBOB	beta - b
17	16	100.0		Н	ATBOG	actin gamma - bovi
18	16	100.0		~	JC5818	æ
19	9/	100.0		Н	ATBOSM	actin, aortic smoo
20	96	100.0	375	-	ATRB	actin, skeletal mu
21	16	100.0		н	ATRIC	
22	16	100.0		Н	A48324	actin beta, cytosk
23	16	100.0		н	ATAX	actin - Acanthamoe
24	9/	100.0		٦	ATCHB	Д
25	9/	100.0		-	ATDO	actin - slime mold
26	9/	100.0		-	ATHUB	actin beta - human
27	9/	100.0		н	ATHUG	actin gamma 1 - hu
28	9/	100.0	375	~	ATMSB	
53	16	100.0	375	ч	ATMSG	actin gamma - mous

	actin gamma, cytos	actin, cytosolic (actin 1 - Pneumocy	hypothetical prote	actin - fission ye	actin beta-2, cyto	actin beta-1, cyto			actin alpha, cardi		actin - Phaffia rh	actin - soybean	actin gamma, cytos	actin - Entamoeba
ATRBB	\$11222	S33386	S47897	T25272	A26836	S71125	S71124	S71126	A55001	A54728	S42103	S70377	ATSY3	A43552	ATAXE
-		~	~	α	7	~	7	~	~	~	~	7	Н	-	ч
375	375	375	375	375	375	375	375	375	375	375	375	375	376	376	376
100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
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ALIGNMENTS

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C. Accession: C43616
R. Paterson, B.M.; Eldridge, J.D.
Softence 224, 1435-1438, 1984
A.Title: alpha-Cardiac actin is the major sarcomeric isoform expressed in embryonic avia A, Reference number: A43616; MUD:84223949; PMID:6729461
A, Accession: C43616
A, Accession: C43616
A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-86 - PAT>
A, Residues: 1-86 - PAT>
A, Residues: 1-86 - PAT>
C, Superfamily: actin
C, Keywords: cytosol; methylated amino acid
F;73/Modified site: 3'-methylhistidine (His) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
actin beta, cytosolic - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 09-Jul-2004
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Pred. No. 7.1e-07;
; Mismatches 0; Indels
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Best Local Similarity 100.0
Matches 15; Conservative
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1 DEAQSKRGILTLKYP 15 ઠે g

actin 5C - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Date: 3D-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004
C;Accession: A28258
R;Vigoreaux, J.O.; Tobin, S.L.
A;Vigoreaux, J.O.; Tobin, S.L.
A;Title: Stage-specific selection of alternative transcriptional initiation sites from the A;Reference number: A28258
A;Accession: A28258
A;Accession: A28258
A;Accession: A28258
A;Residues: 1-137 <VIG>

A;Cross-references: UNIPROT:P10987 A;Note: the authors translated the codon GAG for residue 96 as

 G1

C,Genetics:
A,Gene: FlyBase.Act5C
A,Coses-references: FlyBase.FBgn0000042
C,Superfamily: actin
C,Keywords: methylated amino acid
F,74/Modified site: 3'-methylhistidine (His) #status predicted

100.0%; Score 76; DB 2; Length 137; 100.0%; Pred. No. 1.1e-06; Query Match Best Local Similarity

Gaps

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A;Molecule type: DNA
A;Residues: 1-308 <FYRS-
A;Cross-references: UNIPROT:P02572
A;Note: there are 68 unsequenced residues between positions 160 and 161. Partial sequenc
A;Note: the authors translated the codon GTT for residue 263 as 11e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R,Kang, W.K.; Naya, Y.
Gene 133, 303-304, 1993
AyÎtîle: Sequence of the cDNA encoding an actin homolog in the crayfish Procumbarus clar
A;Reference number: JC2008; WUID:94040829; PMID:8224920
A;Accession: JC2008
                                                                          C,Accession: A61043
K,Bach, R.L.; Jeffery, W.R.
Dev. Genet. 11, 2-14, 1990
A,Title: Temporal and spatial expression of a cytoskeletal actin gene in the ascidian St.
A,Reference number: A61043; MUID:90298580; PMID:2361333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: M0500. "Cyacuston of marthy, R.S.; Davidson, N. Cell 24, 107-116, 1981. Bond, B.J.; Hershey, N.D.; Mixter, K.S.; Davidson, N. Cell 24, 107-116, 1981. Brown of marcin genes of Drosophila: protein coding regions are highly conserved but A;Reference number: A03000; MUID:81210174; PMID:6263481.
                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Residues: 1-213 <BEA>
A,Cross-references: UNIPROT:Q7M3Y7
C,Comment: This sequence is expressed in cells undergoing rapid cell division.
C,Superfamily: actin
C,Keywords: cytoskeleton, methylated amino acid; mitosis; structural protein
F;73/Modified site: 3'-methylhistidine (His) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    actin homolog protein - red swamp crayfish
C;Species: Procambarus clarkii (red swamp crayfish)
C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 20-Jun-2000
C;Accession: JC2008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C,Species: Drosophila melanogaster
C,Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
C;Species: Styela clava
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
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A; Residues: 1-325 <KAN>
A; Cross-references: GB: D14612; NID: 9434784; PIDN: BAA03463.1; PID: 9434785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C.Superfamily: actin
C.Keywords: methylated amino acid
C.Keywords: methylated amino acid
F;74/Modified site: 3'-methylhistidine (His) #status predicted
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100.0%; Score 76; DB 2; I
Best Local Similarity 100.0%; Pred. No. 2.6e-06;
Matches 15; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 76; DB 2; I
Pred. No. 1.8e-06;
                                                                                                                                                                                                                                                                                                               A, Accession: A61043
A, Status: not compared with conceptual translation
A, Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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A;Cross-references: FlyBase:FBgn0000043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0%;
Matches 15; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                     Applies a cardiac actin - mouse (fragment)
C; Species Mus musculus (house mouse)
C; Species Mus musculus (house mouse)
C; Date: 02-U1-1996 #sequence_revision 02-U1-1996 #text_change 09-Jul-2004
C; Date: 02-U1-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C; Date: 02-U1-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C; Accession: 149465; I49465; I49465; MulD:87053822; PMID:3023046
A; Recence number: 149465; MulD:87053822; PMID:3023046
A; Recence number: 149465
A; Status: translated from GB/EMBL/DDBJ
A; Residues: 1-158 cRES>
A; Cross-references: UNIPROT: Q61273; GB:M26775; NID:g191646; PIDN:AAA37165.1; PID:g553858
A; Cross-references: GB:M26776; NID:g191649; PIDN:AAA37166.1; PID:g553859
A; Cross-references: GB:M26776; PIDN:AAA37166.1; PID:g553859
A; Cross-references: GB:M26776; NiD:g191649; PIDN:AAA37166.1; PID:g553859
A; Cross-references: GB:M26776; PIDN:AAA37166.1; PID:g553859
A; Cross-references: GB:M26776; PIDN:AAA37166.1; PID:g553859
A; Cross-references: GB:M26776
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C;Species: Solanum tubersum (potato)
C;Species: Solanum tubersum (potato)
C;Date: 22-Nov-1993 #sequence_revision 17-Oct-1997 #text_change 09-Jul-2004
C;Accession: 820097
J; Mol. Evol. 31, 132-150, 1990
A;Title: Independent gene evolution in the potato actin gene family demonstrated by phyl A;Reference number: 820092; MUID:91012599; PMID:2120451
A;Reference number: 820097
A;Residues: 1-195 < DRA
A;R
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Pred. No. 1.3e-06;
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Pred. No. 1.6e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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         Mismatches
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100.0%; Pre
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Best Local Similarity 100.0%;
Matches 15; Conservative 0
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                                                                                                                                            57 DEAQSKRGILTLKYP 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEAQSKRGILTLKYP 79
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Matches 15; Conservative
                                                                                             DEAQSKRGILTLKYP
         Conservative
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              15;
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Gaps

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the mouse; evolutionary relations
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A;Cross-references: UNIPROT:Q61275; GB:X03767; GB:J00381; GB:M10652; NID:g49869; PIDN:CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C,Accession: S68898

R;McDowell, J.M.; Huang, S.; McKinney, E.C.; An, Y.Q.; Meagher, R.B.

Genetics 142, 587-602, 1996

A;Title: Structure and evolution of the actin gene family in Arabidopsis thaliana.

A;Reference number: S68089; MUID:96158109; PMID:8852856

A;Reference number: S68089

A;Status: not compared with conceptual translation

A;Molecule type: DM.
                                                                                                                                                                                                                                                                                                                                                                  C;Superfamily: actin
C;Keywords: cardiac muscle; heart; methylated amino acid; muscle; skeletal muscle
F;47/Modified site: 3'-methylhistidine (His) #status predicted
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C;Species: Gallus gallus (chicken)
C;Date: 09-Sep-1987 #sequence_revision 09-Sep-1987 #text_change 05-Dec-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     actin 2 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 05-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
                           23-Aug-1987 #sequence_revision 23-Aug-1987 #text_change 09-Jul-2004
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100.0%; Score 76; DB 2; Length 349;
Best Local Similarity 100.0%; Pred. No. 3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels
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C;Superfamily: actin
C;Keywords: cytosol; methylated amino acid
F;74/Modified aite: 3'-methylhistidine (His) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                             RiAlonso, S.; Minty, A.; Bourlet, Y.; Buckingham, M. M. Mol. Bvol. 23, 11-22, 1986
A;Title: Comparison of three actin-coding sequences in the Reference number: A25819; MUID:86200234; PMID:3084797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Accession: A26559
R; Bergsma, D.J.; Chang, K.S.; Schwartz, R.J.
Mol. Cell. Biol. 5, 1151-1162, 1985
A; Reference number: A26559; MUID:85213487; PMID:4000121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 76; DB 2; L. Pred. No. 3.1e-06;
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C, Keywords: cytoskeleton; structural protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-361 <MCD>
A;Cross-references: UNIPROT:Q93ZL9
A;Note: mRNA sequencing was also done
C; Species: Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DEAQSKRGILTLKYP 15
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Best Local Similarity 100.
Matches 15; Conservative
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                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
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                                                                  C; Accession: B25819
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C;Species: Ctenopharyngodon idella (grass carp)

C;Species: Ctenopharyngodon idella (grass carp)

C;Species: O-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004

C;Accession: S05430

R;Liu, Z.; Zhu, Z.; Roberg, K.; Faras, A.J.; Guise, K.S.; Kapuscinski, A.R.; Hackett, P. Nucleic Acids Res. 17, 5850, 1898

A;Title: The beta-actin gene of carp (Ctenopharyngodon idella).

A;Reference number: S05430

A;Reference number: S05430

A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-328 <LIU>
A;Cross-references: UNIPROT:P83751; EMBL:M25013

C;Genetics:
A;Introns: 41/3; 121/3; 268/1

C;Superfamily: actin

C;Superfamily: actin

C;Keywords: cytoskeleton; methylated amino acid

F;73/Modified site: 3'-methylhistidine (His) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            actin (clone 302) - brine shrimp (fragment)
C;Species: Artemia sp. (brine shrimp)
C;Accession: 51452
R;Macias, M.T.; Sastre, L.
Rwacias, M.T.; Sastre, L.
Rymacias, M.T.; Rymacias, Rymacias,
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                                                                                                                                       Length 325;
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100.0%; Pred. No. 2.88-06; Ndels
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B25819
actin, fetal skeletal/adult cardiac muscle - mouse (fragment)
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Pred. No. 2.8e-06;
                                                                                                                                    Score 76; DB 2; I
Pred. No. 2.8e-06;
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                                                                                                                                                                                                                                                                    1 DEAQSKRGILTLKYP 15
                                                                                                                                                                                                                                                                                                                 6 DEAQSKRGILTLKYP 20
A, Experimental source: muscle C, Superfamily: actin C, Keywords: muscle contraction
                                                                                                                                Query Match 100.
Best Local Similarity 100.
Matches 15; Conservative
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Best Local Similarity 100.
Matches 15; Conservative
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A; Reference number: A29664; MUID:87311761; PMID:3114500
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C[Species: Emiliania huxleyi
C[Species: Emiliania huxleyi
C[Species: Emiliania huxleyi
C[Species: 16-Feb-1994 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C[Accession: A37431
R[Bhattacharya, D.; Srickel, S.K.; Sogin, M.L.
Mol. Biol. Evol. 10, 689-703, 1993
A;Title: Isolation and molecular phylogenetic analysis of actin-coding regions from Emil A;Reference number: A37431; MUID: 93330051; PMID: 7687735
A;Contents: CCMP379
A;Status: preliminary
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A2965 --
A29664 --
actin - sea urchin (Strongylocentrotus purpuratus)
C;Species Strongylocentrotus purpuratus (purple urchin)
C;Species Strongylocentrotus purpuratus (purple urchin)
C;Date: 15-Dec-1988 #sequence_revision 30-Sep-1991 #text_change 05-Dec-1997
C;Accession: A29664
R;Crain Jr., W.R.; Boshar, M.F.; Cooper, A.D.; Durica, D.S.; Nagy, A.; Steffen, D. J. Moll. Bvol. 25, 37-45, 1987
A;Title: The sequence of a sea urchin muscle actin gene suggests a gene conversion with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: nucleic acid
A;Residues: 1-365 <BHX.
A;Cross-references: UNIPROT:Q41205; GB:S64188; NID:g404406; PIDN:AAB27626.1; PID:g404407
A;NOte: sequence extracted from NCBI backbone (NCBIN:135711, NCBIP:135712)
C;Superfamily: actin
                                                                                                                                                                                                                                                          C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 05-De-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S68090
R;MoDowell, J.M.; Huang, S.; McKinney, B.C.; An, Y.Q.; Meagher, R.B.
Genetics 142, 587-602, 1996
R;MoDowell, J.M.; Huang, S.; McKinney, B.C.; An, Y.Q.; Meagher, R.B.
A;Title: Structure and evolution of the actin gene family in Arabidopsis thaliana.
A;Reference number: S68099; MUD:96158109; PMID:8852856
A;Accession: S68090
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-362 «MCD>
A;Residues: 1-362 «MCD>
A;Residues: L-362 «MCD>
A;Residues: references: UNIPROT:08LB94
A;Note: mRNA sequencing was also done
C;Genetics:
A;Gene: ACTB
C;Superfamily: actin
C;Keywords: cytoskeleton; structural protein
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100.0%; Score 76; DB 2; I
Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 15; Conservative 0; Mismatches 0;
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                                                              1 DEAQSKRGILTLKYP 15
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A,Accession: A29664
A,Molecule type: DNA
A,Rolecule type: DNA
A,Rossidues: 1-370 <CRA>
A,Cross-references: GB:X05739; GB:X05740; GB:X05741; GB:X05742; GB:X05743
A,Note: the authors translated the codon CAG for residue 260 as Glu
C;Superfamily: actin
C;Keywords: methylated amino acid
F;73/Modified site: 3'-methylhistidine (His) #status predicted
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8, 2005, 10:53:06

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PRELIMINARY;
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Matches 15; Conserv
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061375;
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01-AUG-1998 (
01-JUN-2003 (
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061376 schmidtea p
Q95183 oryctolagus
Q9ttw4 bos taurus
062788 sus scrofa
Q9xex8 bubalus bub
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                                                                                April 8, 2005, 09:58:56; Search time 57.8667 Seconds (without alignments) 132.739 Million cell updates/sec
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             GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd
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Maximum Match 100%
Listing first 45 summaries
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Q8MVNO
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Gapop 10.0 , Gapext 0.5
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76
1 DEAQSKRGILTLKYP 15
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2: uniprot_trembl:*
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seq length: 200000000
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Match Length DB
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32 76 100.0 151 2 Q61274 Q61274 mus musculu 33 76 100.0 151 2 Q9PSV5 Q9P
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ALIGNMENTS

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Gaps
                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Chondrostei, Acipenseriformes, Acipenseridae;
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GO; GO:0005884; C:actin filament; IEA.
GO; GO:0005807; C:chloroplast; IEA.
GO; GO:0003704; F:motor activity; IEA.
GO; GO:0003704; F:motor activity; IEA.
GO; GO:0005706; F:turctural constituent of cytoskeleton; IEA.
InterPro; IPR004000; Actin like.
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Zhaobin Z.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
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75 75
75 AA, 8545 MW, 32F1B8CC7C40E388 CRC64;
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75 AA
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                                         Created)
PRT;
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PROSITE; PS00406; ACTINS_1; 1.
Chloroplast. 1 1
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                                       05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
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79 AA.
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InterPro, IPR004000, Actin_like.
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PROSITE, PS00406; ACTINS_1; 1.
Structural protein.
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Best Local Similarity 100.
Matches 15; Conservative
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Best Local Similarity
Matches 15; Conserv
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                                            Schmidtea polychroa.
Bukaryota, Metazoa, Platyhelminthes, Turbellaria, Seriata, Tricladida,
Paludicola, Dugesiidae, Schmidtea.
NCBI_TaxID=50054;
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Bukaryota, Metazoa, Platyhelminthes, Turbellaria, Seriata, Tricladida,
Paludicola, Dugesiidae, Schmidtea.
                                                                                                                                                  MEDIJNE=98186847; PubMed=9518500; DOI=10.1093/nar/26.8.2031; REGOURTH Cabbiani G., Pascolini R., Neuville P.; Rapbiani G., Pascolini R., Neuville P.; Multiple isoform recovery (MIR)-PCR: a simple method for the isolation of related mRNA isoforms."; Nucleic Acids Res. 26.2031-2033(1998).

-!- FUNCTION: Actins are highly conserved proteins that are involved in various types of cell motility and are ubiquitously expressed in all eukaryotic cells (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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-!-PINCITION: Actins are highly conserved proteins that are involved in various types of cell motility and are ubiquitously expressed in all eukaryotic cells (By similarity).
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GO; GO:0003774; F:mctox activity; IEA.
GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
InterPro; IPR004000; Actin_like.
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EMBL, AF027162; AAC38982.1; -.

EMBL, AF027162; AAC38982.1; -.

GO; GO:000584; C:actin filament; IEA.

GO; GO:0003774; F:motor activity; IEA.

GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.

InterPro; IPR004000; Actin.

EMBL.

PF00022; Actin; 1.
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                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: Belongs to the actin family.
EMBL; AF027161; AAC38981.1; -.
HSSP; P02577; 1NM1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00190; ACTIN.
PROSITE; PS00406; ACTINS_1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00022; Actin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Structural protein.
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Name=DpAct2;
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les 15; Conserv
    Actin 1 (Fragment)
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061376;
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Matches

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Gaps
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 24, Last annotation update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Beta-actin (Fragment)
Deta-actin (Fragment)

Deta-actin (Fragment)

Mammalia, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UMY-2003 (TrEMBLrel. 24, Last annotation update)
Beta actin (Fragment).
Bets actin (Fragment).
Bos taurus (Bovine).
Eukaryota, Metazca, Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
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GO; GO:0003774; F:motor activity; IEA.
GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
                                                   100.0%; Score 76; DB 2; Length 78; 100.0%; Pred. No. 2e-06; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 76; DB 2; Length 79; 100.0%; Pred. No. 2.1e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=22306422; PubMed=12388084;
Wang D.-A., Du H., Jaggar J.H., Brindley D.N., Tigyi G.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
SEQUENCE 78 AA; 8265 MW; B9DFF9B28E4ADB0E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79 AA; 8420 MW; 05056E4E2AC092F8 CRC64;
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Length 82;

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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                     Bovinae, Bubalus.
NCBI_TaxID=89462;
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01-JUN-2003
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Query Match
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                                 Matches
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                                                   MEDLINE=99244362; PubMed=10229356; MEDLINE=99244362; PubMed=10229356; MCDLINE=99244362; PubMed=10229356; MCDLINE=99244362; PubMed=10229356; MCDLINE=9824362; MCDLINE=101; MCDL
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
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GO; GO:0005884; C:actin filament; IEA.
GO; GO:0003774; F:motor activity; IEA.
GO; GO:000500; F:structural constituent of cytoskeleton; IEA.
InterPro; IPR004000; Actin.
InterPro; IPR004000; Actin.
PFam; PF00022; Actin.
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GO; GO:0003774; F:motor activity; IEA.
GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                    80 AA; 9133 MW; 47354ABB7010668D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82 AA; 9410 MW; 8FCC5A5BDAB9F9DC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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PROSITE; PS01132; ACTINS_ACT_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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InterPro; IPR004000; Actin_like.
Pfam; PF00022; Actin, 1.
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PROSITE; PS00406; ACTINS_1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                            80
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Best Local Similarity
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              NCBI_TaxID=9913;
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                   Gaps
                                                                                                                                                                                                                  01-NOV-1999 (TrEMBirel. 12, Created)
01-NOV-1999 (TrEMBirel. 12, Last sequence update)
01-JUN-2003 (TrEMBirel. 24, Last annotation update)
Beta actin (Fragment).
Bubalus bubalis (Domestic water buffalo).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
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GO; GG:0003774; F:motor activity; IEA.
GO; GG:0005200; F:structural constituent of cytoskeleton; IEA.
InterPro; IPR004001; Actin.
InterPro; IPR004001; Actin.
FRAM: PF00022; Actin; 1.
PRINTS; PR00190; ACTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 76; DB 2; Length 82; 100.0%; Pred. No. 2.1e-06; Live 0; Mismatches 0; Indels
                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82 AA; 9417 MW; 9709C6112FAF296C CRC64;
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100.0%; Score 76; DB 2; I
100.0%; Pred. No. 2.1e-06;
iive 0; Mismatches 0;
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PROSITE; PS01132; ACTINS ACT_LIKE; 1.
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MEDLINE=84223949; PubMed=6729461;
Paterson B.M., Eldridge J.D.;
                                   ;
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                                                                     1 DEAQSKRGILTLKYP 15
                                                                                         Local Similarity 100.
                                   15; Conservative
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Gallus gallus (Chicken)
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Boltenia villosa.
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                                           QBMVN0
                               QBMVN0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q86CV4
             RESULT 10
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                     OBMVN0
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McGowan C., Davidson E.A., Davidson W.S.; Submitted (MAR-2003) to the EMBI/Genbank/DDBJ databases.
-!- FUNCTION: ALCIN are highly conserved proteins that are involved in various types of cell motility and are ubiquitously expressed in all eukaryotic cells (By similarity).
-!- SIMILARITY: Belongs to the actin family.
EMBL; AY262761; AAP31127.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                       Beta-actin (Fragment).

Beta-actin (Fragment).

Salvelinus alpinus (Arctic char).

Bukaryota, Metazoa, Chordata, Cramiata, Vertebrata, Buteleostomi,
Actinopterygii, Neoperygii, Teleostei, Buteleostei,

Protacanthopterygii, Salmoniformes, Salmonidae, Salvelinus.
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0
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GO; GO:0003774; F:motor activity; IEA.
GO; GO:0003770; F:motor activity; IEA.
InterPro; IPR004001; Actin.
InterPro; IPR004000; Actin_like.
                                                                                                                                                                                                 100.0%; Score 76; DB 2; Length 86; 100.0%; Pred. No. 2.3e-06; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 91;
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100.0%; Pred. No. 2.4e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91 AA; 10063 MW; 7118DB6663CD895C CRC64;
                                                                                                                                                                            86 AA; 9351 MW; A55285196A328E6E CRC64;
                                                                                                                                                                                                                                                                                                                                    01-JUN-2003 (TrEWBLrel. 24, Last sequence update) 01-MAR-2004 (TrEWBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                           91 AA.
                                                                                                                                                                                                                                                                                                                             01-JUN-2003 (TrEMBLrel. 24, Created)
                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                      PRINTS; PR00190; ACTIN.
PROSITE; PS00406; ACTINS_1; 1.
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PROSITE; PS00406; ACTINS_1; 1.
                                                                                                                                                                                                                                        1 DEAQSKRGILTLKYP 15
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                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 15, Conservative
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                                                                                                                                                           Structural protein.
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Les 15; Conserv
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Q7ZZI1
ID Q7ZZ:
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1 DEAQSKRGILTLKYP 15 |||||||||||||| 54 DEAQSKRGILTLKYP 68

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Gaps
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MEDLINE=22480340; PubMed=12574518; DOI=10.1073/pnas.0336368100;

Mittkopp P.J., Williams B.L., Selegue J.E., Carroll S.B.;

Mittkopp P.J., Williams B.L., Selegue J.E., Carroll S.B.;

"Drosophila pigmentation evolution: divergent genotypes underlying convergent phenotypes.";

Proc. Natl. Acad. Sci. U.S.A. 100:1808-1813(2003).

-!- FUNCTION: Actins are highly conserved proteins that are involved in various types of cell motility and are ubiquitously expressed in all eukaryotic cells (By similarity).
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GO; GO:0003774; F:motor activity; IEA.
GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 94;
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100.0%; Pred. No. 2.5e-06;
Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Urochordata, Ascidiacea,
Stolidobranchia, Pyuridae, Boltenia.
NCBI_TaxID=63515;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94 AA; 10576 MW; 6CEAB58DA12372A4 CRC64;
                                                                    01-007-2002 (TrEMBLrel. 22, Created)
01-007-2002 (TrEMBLrel. 22, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Cytoskeletal actin 2-like protein (Fragment).
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=22248966; PubMed=12361966;
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InterPro; IPR004000; Actin_like.
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PRINTS; PR00190; ACTIN.
PROSITE; PS00406; ACTINS_1; 1.
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Best Local Similarity 100.
Matches 15; Conservative
PRELIMINARY;
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NON TER 94
SEQUENCE 94 AA; 1
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NCBI_TaxID=6999;
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SEQUENCE FROM N.A.

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SEQUENCE FROM N.A.

MILLS 5010-0951.0;

Wittkopp P.J., Williams B.L., Selegue J.E., Carroll S.B.;

Torosophila pigmentation evolution: divergent genotypes underlying convergent phenotypes.";

Proc. Natl. Acad. Sci. U.S.A. 100:1808-1813(203).

- I- FUNCTION: Actins are highly conserved proteins that are involved in various types of cell motility and are ubiquitously expressed in various types of cells (By similarity).

- I- FUNCTION: Actins are highly conserved proteins that are involved in various types of cells (By similarity).

- I- FUNCTION: Actins are highly conserved proteins that are involved in various types of cells (By similarity).

- I- FUNCTION: Actins are highly conserved proteins that are involved in various types of cells (By similarity).

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- I- FUNCTION: Actins are highly conserved proteins that are involved in various types of Cells (By similarity).

- I- FUNCTION: Actins are highly conserved proteins that are involved in various types of Cells (By Section Cells (By similarity).

- I- FUNCTION: With are highly conserved protein filament of cytoskeleton, IEA.
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                                                           GO; GO:0005884; C:actin filament; IEA.
GO; GO:0003774; F:motor activity; IEA.
GO; GO:000500; F:structural constituent of cytoskeleton; IEA.
InterPro; IPR004001; Actin.
InterPro; IPR004000; Actin.
PFam; PF00022; Actin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila americana (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                       Length 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neoptera; Endopterrygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. TaxID=40366;
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Pred. No. 2.5e-06;
                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                      96 AA; 10610 MW; 1454B7D9DD3F3564 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96 AA; 10610 MW; 1454B7D9DD3F3564 CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                   100.0%; Score 76; DB 2; L. 100.0%; Pred. No. 2.5e-06; ive 0; Mismatches 0;
-!- SIMILARITY: Belongs to the actin family.
EMBL; AY165541; AAP21565.1; -.
HSSP; P02568; 1LCU.
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100.0%; Pre
                                              FlyBase; FBgn0066214; Dnov\ActE2.
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InterPro; IPR004000; Actin_like.
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PROSITE; PS00406; ACTINS_1; 1.
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PROSITE; PS00406; ACTINS_1; 1.
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Best Local Similarity 100.
Matches 15; Conservative
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NON TER 96
SEQUENCE 96 AA; 1
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les 15; Conserv
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SEQUENCE
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Ishiwata H., Katsuma S., Kizaki K., Patel O.V., Nakano H.,
Takahashi T., Imai K., Hirasawa A., Shiojima S., Ikawa H., Suzuki Y.,
Tsujimoto G., Izaike Y., Todoroki J., Hashizume K.;
"Characterization of gene expression profiles in early bovine
pregnancy using a custom cDNA microarray.";
Mol. Reprod. Dev. 65:9-18(2003).
-!- FUNCTION: Actins are highly conserved proteins that are involved
in various types of cell motility and are ubiquitously expressed
in all eukaryotic cells (By similarity).
-!- SINILARITY: Belongs to the actin family.
EMBI, AB098074; BAC56464.1; --
HSSP; PO2568; 1P8Z.
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllidae; Gryllinae;
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Zhang H., Shinmyo Y., Hirose A., Mito T., Inoue Y., Ohuchi H.,
Loukeris T.G., Noji S.;
"Extrachromosomal transposition of the transposable element Minos
occurs in embryos of the cricket Gryllus bimaculatus.";
                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae, Bovinae, Bos.

MCBI_TaxID=9913,
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GO; GO:0003774; F:motor activity; IEA.
GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
InterPro; IPR004001; Actin.
InterPro; IPR004000; Actin.like.
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                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=22544902; PubMed=12658628; DOI=10.1002/mrd.10292;
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                                                      01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUAR-2004 (TrEMBLrel. 26, Last annotation update)
Similar to b-actin (Fragment).
Bos taurus (Bovine).
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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100 AA
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PRINTS; PR00190; ACTIN.
PROSITE; PS00406; ACTINS_1; 1.
PROSITE; PS01132; ACTINS_ACT_LIKE; 1.
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PRELIMINARY;
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-I- FUNCTION: Actins are highly conserved proteins that are involved in various types of cell morility and are ubiquitously expressed in all eukaryotic cells (By similarity).

-I- SIMILARITY: Belongs to the actin family.

HNSSP: P10983: 1D4X.
Dev. Growth Differ. 0:0-0(2002).
-!- FUNCTION: Actins are highly conserved proteins that are involved in various types of cell motility and are ubiquitously expressed in all eukaryotic cells (By similarity).
-!- SIMILARITY: BACSS093.1; -.
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Bukaryota, Metazoa, Echinodermata, Eleutherozoa, Echinozoa,
Echinoidea, Euechinoidea, Echinacea, Temnopleuroida, Toxopneustidae,
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                                                                                                                      GO; GO:0005884; C:actin filament; IEA.
GO; GO:0003774; F:motor activity; IEA.
GO; GO:0003700; F:structural constituent of cytoskeleton; IEA.
INTERPRO; IPR004000; Actin.
INTERPRO; IPR004000; Actin.
Pfam; PF00022; Actin.
PROSTIE; PS00406; ACTIN.
PROSTIE; PS00406; ACTIN.
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GO; GO:000384; C:actin filament; IEA.

GO; GO:0003774; F:motor activity; IEA.

GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.

InterPro; IPR004001; Actin.

InterPro; IPR004000; Actin.like.
                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 76; DB 2; Length 104; Best Local Similarity 100.0%; Pred. No. 2.7e-06; Matches 15; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                    104 104
104 AA; 11511 MW; 332777A2B08669B0 CRC64;
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01-07AN-1998 (TrEMBLrel. 05, Last sequence update)
01-07AN-2003 (TrEMBLrel. 24, Last annotation update)
Cytoplasmic actin LvC4 (Fragment).
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PROSITE; PS01132; ACTINS ACT LIKE; 1.
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NON TER 108 10
SEQUENCE 108 AA; 1
                                                                                                           P02577; 1NM1.
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NON TER 104
SEQUENCE 104 AA;
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1 DEAQSKRGILTLKYP 15
          43 DEAQSKRGILTLKYP
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8, 2005, 12:03:12 Search completed: April Job time : 58.8667 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

8, 2005, 09:58:56; Search time 62.4 Seconds (without alignments) 92.971 Million cell updates/sec April Run on:

Title: Perfect score:

US-09-423-351C-10 71 . 1 IQAVLSLYASGRTTG 15

Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

2105692 Total number of hits satisfying chosen parameters:

2105692 segs, 386760381 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_16Dec04:* Database :

genesequ1990s:* genesequ2000s:* genesequ2001s:* genesequ2003s:* genesequ2003as:* genesequ2003bs:* geneseqp1980s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

71 100.0 15 2 AAM12536 Aaw92536 Beta-acti 71 100.0 97 4 AAM12687 Aam26087 Peptide # Abm126087 Abm22618 Peptide # Abm26087 Abm22618 Peptide # Abm26087 Abm26087 Abb22618 Peptide # Abm26087 Abm26087 Peptide # Abm26087 Abb27467 Human pep 77 1 100.0 97 4 AAM58448 Abm26825 Abm26087 Peptide # Abm27087 Abb27467 Human pep 77 1 100.0 97 4 AAM53448 Abm26385 Abm26087 Peptide # Abm27087 Abm27471 Human liv Abm2741 Human liv Abm27471 Human	Result No. Sc	Score	% Query Match	Length	DB	SUMMAKIES	Description
100.0 97 4 AAM13687 Aam13687 Aam13687 Peptic 100.0 97 4 ABB274618 Abb27467 Human 100.0 97 4 ABB27467 Abb27467 Human 100.0 97 4 ABB18116 Abb27467 Human 100.0 97 4 ABB18116 Abb27467 Human 100.0 97 4 ABM5448 Abb281816 Protein 100.0 97 4 ABG47471 Abm2348 Human 100.0 97 4 ABG34659 Human 100.0 97 4 ABG34659 Human 100.0 15 4 ABG3101 Novel 100.0 166 4 ABG2689 Abd35076 Novel 100.0 167 4 ABB66853 Abd35076 Novel 100.0 168 5 ABP42312 Abd2689 Novel 100.0 168 5 ABP42300 Abd2689 Novel 100.0 185 6 ABU70816 Abd370816 Human <t< td=""><td></td><td>71</td><td>100.0</td><td></td><td> ~</td><td>AAW92536</td><td></td></t<>		71	100.0		~	AAW92536	
100.0 97 4 ABB12618 Abb22618 Peptic 100.0 97 4 ABB12467 Abb27467 Abb27471 Abb274771 Abb27471 Abb27471 Abb274771 Abb274771 </td <td></td> <td>71</td> <td>100.0</td> <td>97</td> <td>4</td> <td>AAM13687</td> <td>Peptide</td>		71	100.0	97	4	AAM13687	Peptide
100.0 97 4 AAMASC087 Aama56087 Aama1437 Peptic Aama1437 Aama1437 Aama1437 Aama1437 Aama1437 Aama1437 Aama1437 Aama1448 Aama1437 Aama1437 Aama1448 Aama1437 Aama1448 Aama1448 Aama1448 Aama1448 Aama1448 Aama1448 Aama14		71	100.0	97	4	ABB32618	
100.0 97 4 ABB27467 Abb27467 Human 100.0 97 4 AAMS3448 AamS3448 Human 100.0 97 4 AAMS3448 AamS3448 Human 100.0 97 4 AAM34771 AamS3448 Human 100.0 97 4 AAM313076 Abg35459 Human 100.0 17 4 AAM31076 Abg35459 Human 100.0 150 4 ABG15101 Abg35459 Human 100.0 150 4 ABG66853 Abg35459 Human 100.0 166 4 ABG1689 Abg15101 Novel 100.0 167 ABPA2212 Abg2689 Novel 100.0 168 ABPA2312 Abg159101 Human 100.0 185 ABPA2301 Abg17081 Human 100.0 196 ABPA3101 Abg17081 Human 100.0 204 ABPA3101 Abg37061 Human 100.0 217 ABR73899 Abg37091<		71	100.0	97	4	AAM26087	
100.0 97 4 ABB18116 Abb18116 Protesion 100.0 97 4 AAM55825 Aam65825 Human 100.0 97 4 AAM61848 Aam65484 Human 100.0 97 4 AAM01437 AaM647471 Human 100.0 97 4 AAM01437 AaM647471 Human 100.0 137 4 AAM13076 AaM13076 Human 100.0 150 4 ABG15101 Abg35459 Abg35459 Human 100.0 150 4 ABB66853 Abg26869 Novel Novel 100.0 168 5 ABP42912 Abg26869 Novel Novel 100.0 168 5 ABP42912 Abg26869 Novel Novel 100.0 168 5 ABP42912 Abg26869 Novel Human 100.0 168 5 ABP42912 Abg26869 Novel Human 100.0 168 5 ABP42910 Abg42300 Human 100.0 196 6 ABU70816 Abg470		71	100.0	97	4	ABB27467	
100.0 97 4 AAM55825 Human 100.0 97 4 AAM53448 Aam53448 Human 100.0 97 4 AAM347471 AAM1437 AAM1437 AAM1437 AAM1437 Peptid 100.0 97 4 AAM33076 AAM33076 AAM33076 AAM33076 AAM33076 Novel 100.0 150 4 ABG15101 AAB55853 AAB5559 AAB5559 AAB555101 Novel 100.0 150 4 ABG25869 AAB555101 Novel AAB566853 Drosog 100.0 168 5 ABP42912 AAB566853 Drosog AAB566893 Drosog 100.0 168 5 ABP42912 AAB572912 Human 100.0 183 5 ABP42912 AAB742912 Human 100.0 196 6 ABU70816 AAB73016 AAB73016 AAB73016 AAB73016 AAB73899 AAB73899 AAB73899 AAB73899 AAB73		71	100.0	97	4	ABB18116	
100.0 97 4 AAMS3448 Aam53448 Ham5448 Ham54471 Human 100.0 97 4 AAG47471 AAG35459 Abg35459 Human 100.0 97 5 ABG35459 Abg35459 Human 100.0 137 4 AAG133076 Abg35459 Human 100.0 157 4 ABG455101 Abg355459 Human 100.0 166 4 ABG45101 Abg451510 Novel 100.0 168 5 ABP42212 Abg42512 Abg42512 Human 100.0 185 6 ABU70816 Abu70816 Human Abu70816 Human 100.0 216 5 ABP433016 Human Abu70816 Human 100.0 224 7 ADE31206 Abd33056 Human 100.0 259 7 ABM73899 Abd31206 Human 100.0 257 3 AAG37992 Aag37992 Arab		71	100.0	97	4	AAM65825	Human
100.0 97 4 ABG47471 Abg47471 Human 100.0 97 5 ABG35459 Abg355459 Abg355459 Human 100.0 137 4 AAG13101 Abg355459 Human 100.0 150 4 ABG15101 Abg451510 Novel 100.0 156 4 ABG26869 Abg26869 Novel 100.0 168 5 ABF42912 Abg26869 Novel 100.0 168 5 ABF42910 Abg42912 Abg42304 Human 100.0 183 5 ABF42910 Abg42304 Abg42304 Human 100.0 185 5 ABF42910 Abg42304 Abg42304 Abg42304 Human 100.0 185 5 ABF42910 Abg42301 Abg42304 Abg43304 Abg43304 <td< td=""><td></td><td>71</td><td>100.0</td><td>97</td><td>4</td><td>AAM53448</td><td>Human</td></td<>		71	100.0	97	4	AAM53448	Human
100.0 97 4 AAM01437 Aam01437 Aam01437 Aam01437 Aam01437 Aam01437 Peptid 100.0 197 5 ABG35459 Abg35459 Abg35459 Abg35459 Abg35459 Abg35459 Abg315101 Maman 100.0 150 4 ABG45101 Abg35459 Abg35459 Movel 100.0 168 4 ABG58689 Abg356893 Abg366893 Drosop 100.0 168 5 ABP42912 Abg46883 Abg36869 Novel 100.0 188 5 ABF42912 Abg42912 Abg470816		71	100.0	97	4	ABG47471	Human
100.0 97 5 ABG35459 Abg35459 Human 100.0 137 4 AAU33076 ABG13076 ABG13076 ABG13076 ABG13076 ABG1501 ABG1501 ABG15101 ABG15101 ABG15101 ABG15101 ABG15101 Novel ABG15101 ABG15101 ABG15101 Novel ABG15101 ABG15101 Novel ABG15101 Novel ABG15101 ABG15101 ABG15101 Novel ABG15101 ABG15101 ABG15101 ABG15101 ABG15101 ABG15101 ABG15101 ABG15101 ABG15101 ABG1701 ABG17081 AB		71	100.0	97	4	AAM01437	
100.0 137 4 AAU33076 Aau33076 100.0 150 4 ABG15101 Abg15101 100.0 157 4 ABG6853 Abg26869 100.0 166 4 ABG26869 Abg26869 100.0 168 5 ABP42912 Abg26869 100.0 183 5 ABP42912 Abg42302 100.0 185 6 ABU70840 Abu70840 100.0 196 6 ABU70816 Abu70840 100.0 20 5 ABP43016 Abu70816 100.0 21 7 ABM73899 Aba73389 100.0 239 7 ABE31206 Aba73389 100.0 257 3 AAG20916 Aag37992 100.0 257 3 AAG20916 Aba70649 100.0 274 6 ABU70649 Abu706549		71	100.0	97	ß	ABG35459	Human
100.0 150 4 ABG15101 Abg15101 Abg15101 100.0 157 4 ABB66853 Abb66853 Abb66853 100.0 166 4 ABG26869 Abg26869 100.0 168 5 ABP42310 Abp42310 100.0 185 6 ABU70840 Abu70840 Abu70840 100.0 211 7 ABM73899 Abg3106 Abm73899 100.0 239 7 Abg31206 Abm73899 Ade31206 100.0 257 3 AAG20916 Abu70846 Abm73899 Ade31206 100.0 257 3 AAG20916 Abm73899 Ade31206 100.0 257 3 AAG20916 Abm73899 Ade31206 100.0 257 3 AAG20916 Abm73899 Abm70849		71	100.0	137	4	AAU33076	Novel
100.0 157 4 ABB66853 Abb66653 100.0 166 4 ABG26869 Abg26869 100.0 168 5 ABP4212 Abg4212 100.0 183 5 ABP42300 Abp42310 100.0 185 6 ABU70840 Abb42300 100.0 185 6 ABU70816 Abu70840 100.0 204 5 ABF43016 Abb73016 100.0 231 7 AbF31206 Abc31206 100.0 239 7 Abg31206 Abc31206 100.0 257 3 AAG20916 Abg37992 100.0 257 3 AAG20916 Abd37091 100.0 274 6 ABU70549 Abd70549		71	100.0	150	4	ABG15101	Novel
100.0 166 4 ABG26669 Abg26669 100.0 168 5 ABP42312 Abp42912 100.0 163 5 ABP422912 Abp42301 100.0 183 6 ABU70840 Abp42301 100.0 196 6 ABU70816 Abu70840 100.0 21 7 ABP43016 Abp43016 100.0 21 7 ABM73899 Abm73899 100.0 23 7 ADB31206 Abm73899 100.0 25 3 AAG37992 Abm331206 100.0 25 3 AAG20916 Abm3070549		71	100.0	157	4	ABB66853	
100.0 168 5 ABP42212 Abp42212 Abp42210 100.0 183 5 ABP42210 Abp42300 100.0 185 6 ABU70840 Abu70840 Abu70840 100.0 204 5 ABP43016 Abp43016 Abp43016 100.0 211 7 ABM73899 Abm73899 100.0 239 7 Abm33899 Ade31206 Abm73899 Ade31206 Abm73899 Ade31206 257 3 AAG20916 Abm73899 Ade31206 100.0 257 3 AAG20916 Abm70849 Abm70849 Abm70849		71	100.0	166	4	ABG26869	Novel
100.0 183 5 ABP42200 Abp42200 100.0 185 6 ABU70840 Abu70840 100.0 204 5 ABU70816 Abu70840 100.0 204 5 ABP43016 Abu70816 100.0 211 7 ABM73899 Abm73899 100.0 239 7 Abm31206 Abm73899 100.0 257 3 AAG231992 Aag37992 100.0 257 3 AAG20916 Abu70549 Abu70549		71	100.0	168	Ŋ	ABP42912	Human
100.0 185 6 ABU70840 Abu70840 100.0 196 6 ABU70816 Abu70816 100.0 204 5 ABP43016 Abb73016 100.0 211 7 ABM73899 Abm73899 100.0 239 7 ADE31206 Ade31206 100.0 257 3 AAG20916 Aag37992 100.0 257 3 AAG20916 Abb7320916 100.0 274 6 ABU70549 Abu70549		71	100.0	183	Ŋ	ABP42300	Human
100.0 196 6 ABU70816 Abu70816 100.0 204 5 ABP43016 Abp43016 100.0 211 7 ABM73899 Abm73899 100.0 239 7 ADE31206 Ade31206 100.0 257 3 AAG37992 Aag37992 100.0 257 3 AAG20916 Aag20916 100.0 274 6 ABU70549 Abu70549		7.1	100.0	185	9	ABU70840	Human
100.0 204 5 ABP43016 Abp43016 100.0 211 7 ABM73899 Abm73899 100.0 239 7 ABB31206 Ade31206 100.0 257 3 AAG37992 Aag37992 100.0 257 3 AAG20916 Aag37992 100.0 274 6 ABU70549 Abu70549		71	100.0	196	9	ABU70816	Human
100.0 211 7 ABM73899 Abm73899 100.0 239 7 ADE31206 Ade31206 100.0 257 3 AAG37992 Aag37992 100.0 257 3 AAG20016 Aag20916 100.0 274 6 ABU70549 Abu70549		71	100.0	204	Ŋ	ABP43016	Human
239 7 ADE31206 Ade31206 257 3 AAG37992 Aag37992 257 3 AAG20916 Aag20916 274 6 ABU70549 Abu70549		71	100.0	211	7	ABM73899	_
257 3 AAG37992 Aag37992 257 3 AAG20916 Aag20916 274 6 ABU70549 Abu70549		71	100.0	239	7	ADE31206	-
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.0 274 6 ABU70549 Abu70549 Human		71	100.0	257	m	AAG20916	•
		71	100.0	274	9	ABU70549	Human

Arabidops Arabidops Arabidops Arabidops Human apo Arabidops	
AAGS0947 AAGS0915 AAGS179915 AAGS179916 AAGS179916 AAGS179916 AAGS17209 AAGS17209 AAGS17209 AAGS17209 AAGS17309 AAGS17319 AAGS17319 AAGS17319 AAGS17319 AAGS17319 AAGS17319	
AAGS0947 AAG05115 AAG305115 AAG37991 AAG37991 AAG37990 AAG50914 AAG37209 AAG50945 AAG37209 AAG50945 AAG05113 AAG06449 AAG07390 AAG07390 AAG3731989 AAG37317	
2246 2246 2246 2246 2346 2346 2346 2346	
100000000000000000000000000000000000000	
111111111111111111111111111111111111111	
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	

ALIGNMENTS

RESULT 1

Peptide substrate; CCT; eukaryotic type II chaperonin complex; cyclin; binding agent; substrate-binding site; SBS; substrate folding; actin; tubulin; treatment; cancer; anticancer drug; viral infection; screening; reduced toxicity. Beta-actin reference peptide substrate #10. Ą. AAW92536 standard; peptide; 15 (first entry) 26-APR-1999 AAW92536; AAW92536

WO9853322-A1 26-NOV-1998. Synthetic.

98WO-GB001485. 22-MAY-1998;

(CANC-) INST CANCER RES ROYAL CANCER HOSPITAL. 97GB-00010762. 23-MAY-1997;

Liou AK; Willison K, Hynes G,

WPI; 1999-070162/06.

Identifying specific binding agents for substrate binding site in CCT chaperonin complex - also new peptide binding agents and their mimetics, and peptides containing a specific CCT binding site, used for treating cancer

Disclosure; Fig 10; 97pp; English.

This invention describes a method which uses the CCT (eukaryotic type II chaperonin) complex or part of it, for identifying a binding agent that can occupy a substrate-binding site (SBS) on the CCT complex, the binding agents block an SBS so that biological activity of the CCT complex is affected, particularly its ability to fold substrates such as actin, tubulin and cyclin. The binding agents are useful for treatment of cancer, particularly when used in combination with an anticancer drug, or viral infections. Nucleic acid fragments are used to screen for agents, e.g. binding agents that modulate interaction between the CCT complex and a protein that is to be folded. The binding

8×3335×8

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to human single exon nucleic acid probes (SENP: see AAI10068-AAI28459). The present sequence is a peptide encoded by one such probe. The SENPs are derived from human Hela cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells.
                       90
                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide #121 encoded by probe for measuring cervical gene expression.
                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                        Probe; human; microarray; gene expression; cervical epithelial cell; cervical cancer.
agents may target cells that are actively synthesising tubulin etc. (unlike known microtubule-stabilising agents that affect all cells) should have reduced toxicity for normal cells. AAM92527-W92541 are peptide substrates used in the method of the invention
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                                                                                                                       Length 15;
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                                                                                                                                                       Indels
                                                                                                                     100.0%; Score 71; DB 2; L. 100.0%; Pred. No. 8.2e-06; iive 0; Mismatches 0;
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100.0%; Pred. No. 7.6e-05;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rank DR;
                                                                                                                                                                                                                                                                                                            AAM13687 standard; protein; 97 AA.
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2000US-00608408.
2000US-00632366.
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27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
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                                                                                                                                                                                        1 IQAVLSLYASGRITG 15
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                                                                                                                       Query Match 100.
Best Local Similarity 100.
Matches 15, Conservative
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Best Local Similarity
Matches 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-FEB-2000;
                                                                                       Sequence 15
                                                                                                                                                                                                                                                                                                                                                                               12-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-AUG-2001
                                                                                                                                                                                                                                                                                                                                              AAM13687;
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                                                                                                                                                                                                                                                                          RESULT 2
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The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human feetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genome-derived single exon nucleic acid probes useful for analyzing
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                                                                                                                                                                                                                                                                                                                                                        probe.
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                                                                                                                                                                                                                                                                                                         Peptide #124 encoded by human foetal liver single exon probe.
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100.0%; Pred. No. 7.6e-05;
iive 0; Mismatches 0;
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2000US-0207456P.
2000US-00608408.
2000US-00632366.
2000US-0234687P.
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27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
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                                                                                                                                                                                                                                                             (first entry)
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nes 15; Conservative
                                            15 iOAVLSLYASGRITG
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                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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03-AUG-2000;
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Matches
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ABB32618
ID ABB3
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The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived from manA of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for varifying the expression of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for determining predisposition and/or prognosing breast disease. Gene expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring gene expression, with far less bias than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed second of the control of the printed of the control of the printed of the control of 
                                                                                                                                                                                                                                                                                  New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human breast,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein #115 encoded by probe for measuring heart cell gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                 Claim 27; SEQ ID NO 10435; 327pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; gene expression; heart; microarray; vascular system; cardiovascular disease; hypertension; cardiac arrhythmia; congenital heart disease.
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                                                                                                                                                                                                                                                                                                                                              comprises number of single exon nucleic acid probes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 71; DB 4; I 100.0%; Pred. No. 7.6e-05;
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                                                                                                                                     (MOLE-) MOLECULAR DYNAMICS INC
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03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
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26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
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nes 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human genome-derived single exon nucleic acid probes useful for analyzing
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                                microarray; human; placenta; antenatal diagnosis;
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30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-023468TP.
27-SEP-2000; 2000US-023459P.
04-OCT-2000; 2000GB-00024263.
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2000US-0207456P.
2000US-00608408.
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                                                         genetic disorder
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                                                                                                            Homo sapiens.
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                                                                                                                                         The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart (see ABA21355-ABA41305). The present sequence is a protein encoded by one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the wipo.int/published_pct_sequences
                                                                                                Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; bone marrow expressed exon; gene expression analysis; probe;
microarray; cancer; leukaemia; lymphoma; myeloma.
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                                                                                                                                                                                                                                                                                           Length 97;
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                                                                                                                                                                                                                                                                                              Score 71; DB 4; Pred. No. 7.6e-05;
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                                                                                                                             Claim 15; SEQ ID NO 19886; 530pp; English.
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                                                           DR;
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100.0%;
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03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
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21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
                                                           Chen W,
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26-MAY-2000; 2000US-0207456P.
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Best Local Similarity 100.
Matches 15; Conservative
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                                                           Hanzel DK,
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                                                                                                                                                                                                                                                                           Sequence 97 AA;
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                                                                                                                                                                 probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leuksemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention
Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow.
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Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
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                                                                                                                                           invention provides a number of single exon nucleic acid
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                                                                                       Example 4; SEQ ID NO 26131; 658pp + Sequence Listing; English.
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2000US-00608408.

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21-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-MAY-2000;
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Query Match

Best Loc Matches

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The present invention relates to novel single exon nucleic acid probes (see AA100010-AA110067). The present sequence is a peptide encoded by one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic aetiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative breast diseases and non-carcinoma tumours. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel single exon nucleic acid probe used to measuring gene expression in a human breast.
                                                                                                                                                                                                                              Peptide #119 encoded by probe for measuring human breast gene expression.
                                                                                                                                                                                                                                                                  Probe; human; breast disease; breast cancer; development disorder; inflammatory disease; proliferative breast disease; non-carcinoma tumour.
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100.0%; Pred. No. 7.6e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chen W, Rank DR;
                                                                                                     AAM01437 standard; protein; 97 AA.
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2000US-00608408.
2000US-00632366.
2000US-0234687P.
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15 IQAVLSLYASGRTTG 29
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21-SEP-2000;
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                                                            RESULT 10
AAM01437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a single exon nucleic acid probe (SENP) (1) for measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nucleotide sequences given in the specification (or complements) fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (1) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABG47348-ABG5930 represent human information for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO at from wipo.int/pub/published_pct_sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human adult liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                             Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia; coronary heart disease.
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                     Length 97;
                                                          Indels
                     Score 71; DB 4; I
Pred. No. 7.6e-05;
100.0%; Scc...
100.0%; Pred. No...
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hanzel DK, Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                          Human liver peptide, SEQ ID No 26119.
                                                                                                                                                                                                                                                 ABG47471 standard; peptide; 97 AA.
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tive 0;
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30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00631366.
21-SEP-2000; 2000US-023468PP.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
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                                                                                                     1 IQAVLSLYASGRTTG 15
                                                                                                                                 15 IQAVLSLYASGRITG 29
                                                                                                                                                                                                                                                                                                                                 (first entry)
                                      Local Similarity 100.
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Best Local Similarity 100.
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
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09-AUG-2001

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ABG47471;

ABG47471

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Gaps

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ABG35459

Length 97; 0; Indels

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cancer, chronic obstructive ulmonary disease (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary
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nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exponencial acid probes for measuring gene expression in a sample derived from human lung comprising single exponencial probes having one of from human lung comprising single exponencial probes having one of 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614 complements or the 12387 open reading frames derived from the 12614 complements or the 12387 open reading frames derived from the 12614 comprising the novel set of probes which hybridise at high stringency to a nucleic acid derived from human lung, comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung comprising (a) contacting the array; identifying exons in a eukaryotic genome, comprising (a) algorithmically predicting at least one exon from genomic sequences of the eukaryote; and (b) detecting specific hybridisation of detectably comprising (a) algorithmically predicting at least one exon from genomic sequences of the eukaryote; and (b) detecting specific hybridisation of detectably comprising (a) identifying exons from genomic sequence by the method above mentioned microarray; assigning exons to a single exon comprising (a) identifying exons from genomic sequence by the method above and (b) measuring the expression of each of the exons in the tissues and/or cell types using hybridisation to a single exon compression of the exons in the tissues and/or cell types indicates that the exons should be assigned to a single gene; a peptide comprising one of 12011 sequences, mentioned in the specification, or encoded by the cyrpession of the exons in the tissues and/or cell types in dentifying exons in a gene, particularly using human constructive pherived malysis, and for identifying exons in a gene, particularly using human construction whences, mentioned described manalysis and for identifying exons in a gene, com
                                                                            Human peptide encoded by genome-derived single exon probe SEQ ID 25124.
                                                                                                                                                                   Human; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease; Hermansky-Pudlak syndrome; sarcoidosis; pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; primary dyshinesis; pulmonary hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Spatially-addressable set of single exon nucleic acid probes, used to measure gene expression in human lung samples.
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30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-023669P2.
27-SEP-2000; 2000US-0236359P.
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(first entry)
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The invention relates to novel human secreted polypeptides. The polypeptides are useful for determining the presence of or predisposition to a disease associated determining the presence of or predisposition to a disease associated determining the presence of or predisposition to a disease associated comparing the proteins are useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for useful interactions of the polypeptides and cells genetically engineered nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins can useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They way be used to increase stem cell proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon can and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. AAU29510-AAU33104 represent the amino acid sequences of novel human
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histiocytosis, lymphangioleiomyomtosis, pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary dyskinesis, pulmonary hypertension and hyaline membrane disease. The present sequence is a peptide/protein enroceded by a single exon probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            stem cell proliferation; haematopoiesis; nerve tissue regeneration; immune suppression; immune stimulation; anti-inflammatory; leukaemia.
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                                                                                                                                                                                                    100.0%; Score 71; DB 5; L 100.0%; Pred. No. 7.6e-05;
                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                      AAU33076 standard; protein; 137 AA.
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26-JAN-2001; 2001US-00770160
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Best Local Similarity 100.
Matches 15; Conservative
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                                                                                                                                                                  Sequence 97 AA;
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                                    Matches
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ABB66853
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal cativity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in issue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG00010. Note: The sequence data for this mino acid sequences of the invention. Note: The sequence data for this electronic format directly from MNPO at the printed specification, but was obtained in electronic format directly from MNPO at the printed specification, but was obtained in electronic format directly from MNPO at
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                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                        Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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                                    Length 137;
                                                                          Indels
                  Score 71; DB 4; Len
Pred. No. 0.00012;
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                                                                                                                                                                                                                                                                                                                                                                 Novel human diagnostic protein #15092.
                                                                                                                                                                                                                                                   ABG15101 standard; protein; 150 AA.
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                                    100.0%;
100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
                                                                                                                15
                                                                                                                                      80 IQAVLSLYASGRTTG 94
                                                                          Conservative
                                                                                                                1 IQAVLSLYASGRITG
                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-639362/73.
N-PSDB; AAS79288.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HYSE-) HYSEQ INC.
Sequence 137 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 150 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              biodiversity.
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                                                                                                                                                                                                                                                                                                                             18-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-OCT-2001.
                                                                                                                                                                                                                                                                                       ABG15101;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila, developmental biology, cell signalling, insecticide;
                                                       o;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 27351; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 71; DB 4; Length 157; 100.0%; Pred. No. 0.00014; ive 0; Mismatches 0; Indels
100.0%; Score 71; DB 4; Length 150; 100.0%; Pred. No. 0.00013;
                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster polypeptide SEQ ID NO 27351
                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABG26869 standard; protein; 166 AA.
                                                                                                                                                                                                                                                                                                 ABB66853 standard; protein; 157 AA.
        100.0%; Fr. 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-MAR-2001; 2001WO-US009231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
                                                                                                                                             98 IQAVLSLYASGRITG 112
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                                                                                                            1 IQAVLSLYASGRTTG 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2001-656860/75.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 157 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200171042-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pharmaceutical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABG26869
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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restrore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and ite binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                  Human, chromosome mapping, gene mapping, gene therapy, forensic; food supplement, medical imaging; diagnostic, genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 20; SEQ ID NO 57228; 103pp; English.
                                                         Novel human diagnostic protein #26860.
                                                                                                                                                                                                                                                                                                                                    31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Drmanac RT, Liu C, Tang YT;
                                                                                                                                                                                                                                                                                             30-MAR-2001; 2001WO-US008631.
                   18-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-639362/73.
N-PSDB; AAS91056.
                                                                                                                                                                                                                                                                                                                                                                                                    (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 166 AA;
                                                                                                                                                                                                          WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                biodiversity.
                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                   11-0CT-2001.
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Gaps ; 0 Query Match
100.0%; Score 71; DB 4; Length 166; Best Local Similarity 100.0%; Pred. No. 0.00015; Matches 15; Conservative 0; Mismatches 0; Indels

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Search completed: April 8, 2005, 10:50:48 Job time : 62.4 secs g

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

8, 2005, 09:58:57; Search time 17.5333 Seconds (without alignments) 63.863 Million cell updates/sec April Run on:

Perfect score:

US-09-423-351C-10 71 1 IQAVLSLYASGRITG 15 Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

513545 seqs, 74649064 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

/cgn2_6/ptodata/1/iaa/SA_COMB.pep:*
/cgn2_6/ptodata/1/iaa/SB_COMB.pep:*
/cgn2_6/ptodata/1/iaa/GA_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RB_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:* Issued Patents AA:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match 100.0	Length 336 371	DB - 4	ID US-09-248-796A-14108 US-08-261-206A-77	Description Sequence 14108, A Sequence 77, Appl
0 M 4 n	1771	0.000	371 374 375	- m 07 r	US-08-261-206A-77 US-08-609-236-6 US-08-494-114	14,
00700	1222	00000	375 375 375	ი ო ო •	US-09-100-217-15 US-09-171-337A-7 US-09-171-337A-8 US-09-631-022-7	9, 6, 6, 6
1212	12221	100.00	376 376 376	・414	09-976-594 08-588-113 09-949-016	233
115	7777	1000.0	377 377 386 399	0 4 4 4 4	US-09-1106-21/-2 US-09-919-172-33 US-09-917-254-53 US-09-949-016-7721 US-09-949-016-9424	Sequence 2, Appli Sequence 33, Appl Sequence 53, Appl Sequence 7721, Ap
3227038	711 711 68 65 65	95.00 95.00 95.8 91.5 91.5		. 4 4 4 A W 4 W	US-09-949-016-10757 US-09-949-016-11313 US-09-348-796A-14109 US-09-306-446C-5 US-09-306-446C-2	10757, 11313, 14109, 5, App 7725, 2, App
25 25 27	6 6 5 6 5 7 8	91.5 91.5 91.5 91.5	376 376 376 376	4444	US-09-538-092-1109 US-09-538-092-1110 US-09-949-016-6656 US-09-949-016-8452	Sequence 1109, Ap Sequence 1110, Ap Sequence 6656, Ap Sequence 8452, Ap

395, App	6655, Ap	7396, Ap	3, Appli	Appli	Appli	Appli	, Appl	, Appl	6906, Ap	39072, A	54289, A	I, Appl	, Appl	ı, Appl	, Appl	', Appl	', Appl
		73					72	72			24	43	43	43	43	4	47
Sequence	Seguence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
US-09-538-092-395	US-09-949-016-6655	US-09-949-016-7396	US-09-428-517-3	US-09-428-517-2	US-09-697-022-4	US-09-697-022-5	US-09-410-551B-72	US-09-940-316B-72	US-09-107-532A-6906	US-09-270-767-39072	US-09-270-767-54289	US-09-245-281-43	US-09-207-359B-43	US-09-340-620A-43	US-09-865-364-43	US-09-207-359B-47	US-09-865-364-47
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87.3	71	71	62	62	54	54	54	54	53.5	23	53	23	23	23	53	23	53
62	51	51	44	44	39	39	39	39	38	38	38	38	38	38	38	38	38
28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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Sequence 14108, Application US/09248796A

Sequence 14108, Application US/09248796A

Patent No. 6747137

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US 60/074,725

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR FILING DATE: 1998-02-13

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 14108

LENGTH: 336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 71; DB 4; Length 33.
Pred. No. 7.6e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Sc
100.0%; Pr
tive 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 IOAVLSLYASGRITG 15
                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT; ORGANISM: Candida albicans
US-09-248-796A-14108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.
Best Local Similarity 100.
Matches 15, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δ
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69 iQAVLSLYASGRITG 83 g

APPLICANT: Zushi, Mitichitaka
APPLICANT: Gomi, Komakazu
APPLICANT: Gomi, Komakazu
APPLICANT: Yanamoto, Shuji
APPLICANT: Suzuki, Koji
APPLICANT: Suzuki, Koji
APPLICANT: Matsuda, Akio
TITLE OF INVENTION: A Polypeptide Capable of Interacting
TITLE OF INVENTION: With Thrombin
NUMBER OF SEQUENCES: 80
CORRESPONDENCES. B0
CORRESPONDENCES. B1cch, Stewart, Kolasch & Birch
STREET: 301 N. Washington St.
CITY: Palls Church
STRATE: Virginia
COUNTRY: USA Sequence 77, Application US/08261206A; Patent No. 5574007; GENERAL INFORMATION: US-08-261-206A-77 RESULT 2

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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 374;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 14, Application US/08494151

Patent No. 5840528

JERERAL INFORMATION:
APPLICANT: Van Ooyen, Albert Johannes Joseph
TITLE OF INVENTION: Transformation of Phaffia rhodozyma
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mortison & Foerster
STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 71; DB 3; I
Best Local Similarity 100.0%; Pred. No. 8.6e-05;
Matches 15; Conservative 0; Mismatches 0;
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Best Local Similarity 100.C
Matches 15; Conservative
                                                                                                                                                          MOLECTLE TYPE:
DESCRIPTION: Protein
HYPOTHETICAL: No
ANTI-SENSE: No
FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 2000 Pennsylva CITY: Washington, D.C.
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein US-08-494-151-14
                                                                                                                                                                                                                                                                                                                                                INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
TOPOLOGY: linear
                                                                                                       STRANDEDNESS:
TOPOLOGY: Linear
                                                                                 TYPE: Amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                              CELL TYPE:
; CELL LINE:
US-08-609-236-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-494-151-14
                                                                                                                                                                                                                                                                                                                            STRAIN:
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JAPLICANT: Steven R. Goodman

TITLE OF INVENTION: No. 6087398el Sickle Cell Anemia Treatment

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:
ADDRESSEE: McGregor & Adler, LLP
STREET: 8011 Candle Lane
CITY: Houston
STRATE: Texas
COUNTRY: USA
ZIP: 77071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
SOFTWARE: Microsoft Word for Word For Microsoft Word For Word
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
  ZIP: 22046-0747

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/261,206A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 71; DB 1; 1
Pred. No. 8.5e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                      PEPLICATION NOTE.

FILING DATE:
CLASSIPLICATION: 530

PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/740,492
FILING DATE: 03-40G-1991
ATTORNEY/AGENT INFORMATION:
NAME: Svenseon, Leonard R.
REGISTRANICN NUMBER: 30330
REFERENCE/DOCKET NUMBER: 216-275P
TELEPHONE: 703-241-1300
TELEPHONE: 703-241-2848
TELEPHONE: 703-241-2848
TELEPHONE: 703-241-2848
TELEPHONE: 713-241-2848
TELEFACOMUNICATION INFORMATION: 77:
SEQUENCE CHARACTERISTICS:
LENGTH: 371 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: APPLICATION: Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/ACENT INFORMATION:
NAME: Benjamin Azron Adler, Ph.D.
REGISTRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D5807
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-777-6908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/08609236
Patent No. 6087398
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Best Local Similarity 100.09
Matches 15; Conservative
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US-08-609-236-6
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US-09-171-337A-8
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                                                                                    US-09-106-217-16

1 Sequence 16, Application US/09106217

2 Sequence 16, Application US/09106217

3 GENERAL INFORMATION:

4 APPLICANT: Reating, Mark T.

APPLICANT: Olson, Timothy M.

7 TITLE OF INVENTION: Cardiomyopathy, a Heritable Form of Heart Failure

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.

STREET: Tower

CITY: Washington

STREET: DC

COUNTRY: U.S.A.

COUNTRY: U.S.A.
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Sequence 7, Application US/09171337A
Patent No. 6300095
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: BARREDO FUENTE, Jose Luis
RODRIGUEZ SAIZ, Marta
COLLADOS DE LA VIEJA, Alfonso J.
MORENO VALLE, Migenil Angel
SALTO MALDONADO, Francisco
DIEZ GARCIA, Bruno
TITLE OF INVENTION: PROMOTERS OF THE GENES GLUTAMATE
AND -ACTIN AND THEIR USE IN FILAMENTOUS
FUNGI EXPRESSION, SECRETION AND ANTISENSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/106,217 FILING DATE:
CLASSIFICATION:
NAME: Saxe, Stephen A.
REGISTRATION NUMBER: 38,609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 71; DB 3; I
Pred. No. 8.6e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: LADAS & PARRY
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-783-6040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 202-783-003.
INFORMATION FOR SEQ ID NO: 16: SEQUENCE CHARACTERISTICS: LENGTH: 375 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0%;
Matches 15; Conservative 0;
136 IQAVLSLYASGRTTG 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-106-217-16
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US-09-171-337A-7
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Gaps
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COMPUTER: 1EM PC compatible
COMPUTER: 1EM PC compatible
COMPUTER: 1EM PC compatible
OPERATING SYSTEM: Microsoft Windows
SOFTWARE: Worderfect 8 for Windows
SOFTWARE: Worderfect 8 for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/171,337A
FILING DATE: 14-May-1999
CLASSIFICATION S36
PRIOR APPLICATION NUMBER: ES9700482
FILING DATE: 5-WAR-1998
APPLICATION NUMBER: ES9700482
FILING DATE: 5-WAR-1997
ATTORNEY AGENT INFORMATION:
NAME: MASS, Clifford J.
REGISTRATION NUMBER: 30,086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DESHYDROGENASE, -N-ACETYLHEXOSAMINIDASE
AND -ACTIN AND THEIR USE IN FILAMENTOUS
FUNGI EXPRESSION, SECRETION AND ANTISENSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      U-011948-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 71; DB 3; Length 375; 100.0%; Pred. No. 8.6e-05; Live 0; Mismatches 0; Indels
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DIEZ GARCIA, Bruno
TITLE OF INVENTION: PROMOTERS OF THE GENES GLUTAMATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (C) REF./DOCKET NO.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8, Application US/09171337A
Patent No. 6300095
GENERAL INFORMATION:
APPLICANT: BARREDO FUENTE, Jose Luis
RODRIGUEZ SAIZ, Marta
COLLADOS DE LA VIEJA, Alfonso J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Penicillium chrysogenum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
SEQUENCE DESCRIPTION: SEQ ID NO: 7
US-09-171-337A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: LADAS & PARRY
STREET: 26 WEST 61 STREET
CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 233288
INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acids
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          136 IQAVLSLYASGRITG 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 IQAVLSLYASGRITG 15
                                                                  ZIP: 10023
COMPUTER READABLE FORM:
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MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0
Matches 15; Conservative
CITY: NEW YORK STATE: NY
                                                USA
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STATE: NY
COUNTRY: USA
ZIP: 10023
COMPUTER READABLE FORM:
MEDIUM TYPE: 3-1/4" Disk 1.44MB
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Microsoft Windows
CURRENT APPLICATION DATA:
APPLICATION UNDER: US/09/631,022
FILING DATE: 02-Aug-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8, Application US/09631022

Patent No. 6558921

GENERAL INFORMATION

ROBIGUEZ SAIZ, Marta

COLLADOS DE LA VIEJA, Alfonso J.

MORENO VALLE, Migeul Angel

SALTO MALDONADDO, Francisco

DIEZ GARCIA, Bruno

TITLE OF INVENTION: PROMOTERS OF THE GENES GLUTAMATE
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CORRESPONDENCE ADDRESS:
ADDRESSEE: LADAS & PARRY
STREET: 26 WEST 61 STREET
CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DIEZ GARCIA, Bruno
TITLE OF INVENTION: PROMOTERS OF THE GENES GLUTAMATE
DESHYDROGENASE, N-ACETYLHEXOSAMINIDASE
AND -ACTIN AND THEIR USE IN FILAMENTOUS
FUNGI EXPRESSION, SECRETION AND ANTISENSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 10023
COMPUTER READABLE FORM:
MEDIUM TYPE: 3-1/4" Disk 1.44MB
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Microsoft Windows for Workgroups 3.11
SOFTWARE: WordPerfect 8 for Windows
                                       COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CORPERATING SYSTEM: Microsoft Windows
SOFTWARE: Warderfect 8 for Windows
CURRENT APPLICATION DATA:
FILING DATE: 14-May-1999
CLASSIFICATION: 336
                                                                                                                                                                                                                                                                                                                                                                                    U-011948-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7, Application US/09631022
Patent No. 6558921
GENERAL INFORMATION:
APPLICANT: BARREDO FUENTE, Jose Luis
RODRIGUEZ SAIZ, Marta
RODRIGUEZ SAIZ, Marta
MORENO VALLE, MIGENI Angel
SALTO MALDONADO, Francisco
                                                                                                                                                                                          PRIOR APPLICATION: 53.2

PRIOR APPLICATION NUMBER: PCT/ES98/00056

FILING DATE: 5-MAR-1998

APPLICATION NUMBER: ES9700482

FILING DATE: 5-MAR-1997

ATTORNEY/AGENT INFORMATION:

NAME: MASS, Clifford J.

REGISTRATION NUMBER: 30,086
COMPUTER READABLE FORM:
MEDIUM TYPE: 3-1/4" Disk 1.44MB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Acremonium chrysogenum
                                                                                                                                                                                                                                                                                                                                                                                                     TELECONMUNICATION INFORMATION:
TELEPHONE: 233288
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: LADAS & PARRY
STREET: 26 WEST 61 STREET
CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 375 amino acids
TYPE: amino acids
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   136 IQAVLSLYASGRTTG 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 IQAVLSLYASGRTTG 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-171-337A-8
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US-09-631-022-7
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DESHYDROGENASE, -N-ACETYLHEXOSAMINIDASE AND -ACTIN AND THEIR USE IN FILAMENTOUS FUNGI EXPRESSION, SECRETION AND ANTISENSE

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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: amino acid sequence of the protein with a molecular weight of
                                                           APPLICATION NUMBER: 09/171,337
FILING DATE: 14-MAY-1999
APPLICATION NUMBER: PCT/ES98/00056
FILING DATE: 5-MAR-1998
APPLICATION NUMBER: ES9700482
FILING DATE: 5-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: MASS, Clifford J.
REGISTRATION NUMBER: 30,086
REGISTRATION NUMBER: 30,086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      red. No. 8.6e-05;
Mismatches 0;
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100.0%; Score 71; DB 4;
Best Local Similarity 100.0%; Pred. No. 8.6e-05
Matches 15; Conservative 0; Mismatches n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Penicillium chrysogenum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41760 Da.
SEQUENCE DESCRIPTION: SEQ ID NO: 7
FILING DATE: 02-Aug-2000
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acids
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          136 IQAVLSLYASGRTTG 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 IQAVLSLYASGRITG 15
                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
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Sequence 6100, Application US/09949016
; Sequence 6100, Application US/09949016
; Patent No. 6012339
; GENERAL INFORMATION:
; APPLICANT: VENTER, V. Craig et al.
APPLICANT: VENTER, V. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REPREENCE: CLOON 307
; CURRENT APPLICATION NUMBER: 06/241, 755
; CURRENT PILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237, 768
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; RIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FREESEQ for Windows Version 4.0
; SEQ ID NO 6100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                  GENERAL INFORMATION:
APPLICANT: MCHUGH, Kirk M.
TITLE OF INVENTION: DAGNOSTIC TEST FOR DETERMINING
TITLE OF INVENTION: MALIGNANCY OF SMOOTH MUSCLE TUMORS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
ADDRESSEE: Wo. 5710003ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/588,113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION: 436
FILING DATE:
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Ralph, Rebecca L.
REGISTRATION NUMBER: 35,152
REPRENCE/DOCKET NUMBER: TJU-1652
TELECOMMUNICATION INFORMATION:
                        Sequence 2, Application US/08588113 Patent No. 5710003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  137 IQAVLSLYASGRITG 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 IQAVLSLYASGRITG 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 376 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: protein US-08-588-113-2
                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
GY: linear
                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 19103
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US-09-949-016-6100
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                                                                                                                                                                                                                                                                                                            STATE: PA
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Sequence 731, Application US/09976594
Sequence 731, Application US/09976594
Sequence 731, Application US/09976594
Sequence 731, Application US/09976594
GENERAL INFORMATION:
APPLICANT: Furness, Michael
APPLICANT: Buchbinder, Jenny
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
FILE REFERENCE: PA-0041 US
CURRENT APPLICATION UNMBER: 06/240,409
PRIOR APPLICATION NUMBER: 60/240,409
PRIOR APPLICATION NUMBER: 60/240,409
PRIOR SEQ IN OSS: 1143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             i.
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Pred. No. 8.6e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: amino acid sequence of the protein with a molecular weight of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                           FILING DATE: 3-1-2.
ATTORNEY/AGENT INFORMATION:
NAME: MASS, Clifford J.
REGISTRATION NUMBER: 30,086
(C) REF./DOCKET NO.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 1837317CD1
US-09-976-594-731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
100.0%; Score 71; DB 4; I
Best Local Similarity 100.0%; Pred. No. 8.6e-05;
Matches 15; Conservative 0; Mismatches 0;
                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/171,337
PILING DATE: 14-MAY-1999
APPLICATION NUMBER: PCT/ES94/00056
FILING DATE: 5-MAR-1998
APPLICATION NUMBER: ES9700482
FILING DATE: S-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Acremonium chrysogenum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE DESCRIPTION: SEQ ID NO: 8
                                                                                                                                                                                                                                                                                                       INFORMATION FOR ESQ 1D NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acids
TYPE: amino acids
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Peptide
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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100.0%;
CLASSIFICATION: 536
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Best Local Similarity 100.
Matches 15; Conservative
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LENGTH: 375
TYPE: PRT
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US-09-949-016-6100

RESULT 11

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TYPE: PRT ORGANISM:

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TYPE: PRT
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APPLICANT: Keating, Mark T.
APPLICANT: Keating, Mark T.
TITLE OF INVENTION: Actin Mutations in Dilated
TITLE OF INVENTION: Cardiomyopathy, a Heritable Form of Heart Failure
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
STREET: STREET: SSS THIRTEENTH Street, N.W., Suite 701 East
STREET: Tower
CITY: Washington
STRATE: DC
CONNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: DATENT RELEASE FORM:
MEDIUM TYPE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/106,217
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                     Length 376;
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100.0%; Score 71; DB 3; L
Best Local Similarity 100.0%; Pred. No. 8.7e-05;
Matches 15; Conservative 0; Mismatches 0;
                   Score 71; DB 4;
Pred. No. 8.7e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 33, Application US/09919172
Fatent No. 6673545
GBNEAL INFORMATION:
APPLICANT: Faris, Mary
APPLICANT: TUTHER, Christopher M.,
TITLE OF INVENTION: PROSTATE CANCER MARKERS
FILE REPERENCE: PA-0036 US
CURRENT PILING DATE: 2011-07-30
PRIOR APPLICATION NUMBER: 06/222,469
                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Saxe, Stephen A.
REGISTRATION NUMBER: 38,609
REFERENCE/DOCKET NUMBER: 2323-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-783-6040
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                       Sequence 2, Application US/09106217
Patent No. 6063576
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                   100.0%;
100.0%;
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                                                                                            1 IQAVLSLYASGRTTG 15
Query Match
Best Local Similarity luv..
Thes 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-919-172-33
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Gaps
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APPLICANT: Mutter, George
APPLICANT: Baak, Jan
TILLE OF INVENTION: PCOGNOSTIC Classification of Breast Cancer
TILLE OF INVENTION: PCOGNOSTIC Classification of Breast Cancer
FILE REFERENCE: B0801/7224(JRV)
CURRENT PRILING DATE: 2001-07-27
CURRENT PILING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: US 60/222,093
PRIOR PILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 102
SOFTWARE: Patentin version 3.0
SEQ ID NO 53
LENGTH: 377
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Pred. No. 8.7e-05;
; Mismatches 0; Indels
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                                                                                                                                                     FEATURE:

NAME/KEY: misc feature

CTHER INFORMATION: Incyte ID No. 6673545 1709118CD1
US-09-919-172-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: April 8, 2005, 12:07:38 Job time : 18.5333 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
US-09-317-254-53
Gequence 53, Application US/09917254
Patent No. 6703204
                                                                                                                                                                                                                                                                          Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 15; Conservative 0
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Best Local Similarity 100.0%;
Matches 15; Conservative (
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PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 102
SOFIWARE: PERL Program
SEQ ID NO 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 IOAVLSLYASGRITG 15
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US-09-917-254-53
                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
                                                                                            LENGTH: 377
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April 8, 2005, 10:53:18 ; Search time 42.6667 Seconds (without alignments) 116.718 Million cell updates/sec
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2: /cgn2_6/ptodata/1/pubpaa/NEOT_BW_PUB.pep:*
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19: /cgn2_6/ptodata/1/pubpaa/USIOT_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1418010 segs, 331997259 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                       OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                       US-09-423-351C-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                   Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Searched:
                                                                                                                                                                                                                               Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	Score	Query Match	Query Match Length DB	DB	ID	Description	
	71	100.0	97	6	US-09-864-761-33414	Sequence 33414, A	
7	71	100.0		15	US-10-264-049-4044	Sequence 4044, Ap	
m	71	100.0	180	16	US-10-437-963-169247	Sequence 169247,	
4	71	100.0		15	US-10-264-049-3432	Sequence 3432, Ap	
S	71	100:0		15	US-10-424-599-280810	Sequence 280810,	
9	71	100.0	- ,	15	US-10-264-049-4148	Sequence 4148, Ap	
7	71	100.0		15	US-10-424-599-282905	Sequence 282905,	
æ	7.1	100.0	•	14	US-10-002-631C-56	Sequence 56, Appl	
σ	71	100.0		16	US-10-767-701-42770	Sequence 42770, A	
10	71	100.0		15	US-10-424-599-206389	Sequence 206389,	
11	71	100.0	- •	15	US-10-424-599-143226	Sequence 143226,	
12	71	100.0	248	15	US-10-424-599-162684	Sequence 162684,	
13	71	100.0	•	16	US-10-767-701-43575	Sequence 43575, A	

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44494	69353,	17753	52089	57500	27843			283333,		68,	93, Aj	88, A	2436,		94, A	82, A	101,	17991	20242	45677, 1	46090, A	33, Appl	52, A	64, A	16200	16268	16268	-	22349	m	66124
Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence					Sequence	Sequence	Sequence	Sequence	Seguence 33	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
US-10-425-114-44494	US-10-425-114-69353	US-10-424-599-177530	US-10-425-114-52089	US-10-425-114-57500	US-10-424-599-278431	US-10-425-114-62158	US-10-425-114-59172	US-10-424-599-283333	US-10-128-714-3002	US-10-322-281-68	US-10-205-194-93	US-10-316-253-88	0-369-493-243	US-10-369-493-5927	US-10-205-331-94	US-10-260-708-82	US-10-341-434-101	US-10-437-963-179917	US-10-437-963-202420	US-10-767-701-45677	US-10-767-701-46090	US-09-919-172-33	US-10-338-777-52	US-10-236-031B-64	US-10-424-599-162009		US-10-424-599-162686	US-10-424-599-222816	US-10-424-599-223492	599-28333	US-10-425-114-66124
15	15										14	14	15	15	15	15	15	16	16	16	16	ص ص	14	15	15	15	15	15	15	15	15
250	254	261	276	288	299	313	331	347	355	371	375	375	375	375	375	375	376	376	376	376	376	377	377	377	377	377	377	377	377	377	377
100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
71	71	71	71	71	71	71	71	71	71	71	71	71	71	71	71	71	71	71	71	71	71	71	71	71	71	7.1	71	71	71	71	71
14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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95-09-864-761-33414, Application US/09864761
| Patent No. US2002004896341
| Patent No. US2002004896341
| GRENEAL INFORMATION:
| APPLICANT: Panch, David R. |
| APPLICANT: Rank, David R. |
| APPLICANT: Hardel, David R. |
| APPLICANT: Hardel, David R. |
| APPLICANT: Hardel, David R. |
| TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY |
| TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY |
| TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY |
| TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY |
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| TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY |
| TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY |
| PRIOR PILICATION NUMBER: US 60/230,366 |
| PRIOR PILICATION NUMBER: US 60/236,359 |
| PRIOR PILICATION NUMBER: US 60/236,359 |
| PRIOR PILICATION NUMBER: PCT/USO1/00669 |
| PRIOR PILICATION NUMBER: PCT/USO1/00669 |
| PRIOR PILICATION NUMBER: PCT/USO1/00669 |
| PRIOR PILICATION NUMBER: PCT/USO1/00665 |
| PRIOR PILICATIO
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us-09-423-351c-10.rapb

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N: EXPRESSED IN HEART, SIGNAL = 48
N: EXPRESSED IN BONE MARROW, SIGNAL = 28
N: EXPRESSED IN DULT LIVER, SIGNAL = 24
N: EXPRESSED IN PLACENTA, SIGNAL = 34
N: EXPRESSED IN HB1100, SIGNAL = 95
N: EXPRESSED IN HB1100, SIGNAL = 78
N: EXPRESSED IN HB1100, SIGNAL = 78
N: EXPRESSED IN LUNG, SIGNAL = 45
N: EXPRESSED IN LUNG, SIGNAL = 45
N: EXPRESSED IN LUNG, SIGNAL = 40
N: EXPRESSED IN HELA, SIGNAL = 40
N: EXT_HUMAN HIT: BE21130.1, EVALUE 4.00e-50
N: SMISSPROT HIT: 042161, EVALUE 4.00e-50
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) Sequence 4044, Application US/10264049

Sequence 4044, Application US/10264049

Sequence 6104

Publication No. US20040005579A1

APPLICANT: Birse et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REFERENCE: PA1371

CURRENT APPLICATION NUMBER: US/10/264,049

CURRENT APPLICATION NUMBER: US/10/264,049

PRIOR FILING DATE: 2002-10-04

PRIOR PRILOG DATE: 2001-06-07

PRIOR FILING DATE: 2000-06-07

PRIOR FILING DATE: 2000-06-07

NUMBER OF SEQ ID NOS: 4360

SOFTWARE: PATCHILIN Ver. 3.1
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100.0%; Score 71; DB 15; Length 168;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 15; Conservative 0; Mismatches 0; Indels
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100.0%; Score 71; DB 9; Length 97;
Best Local Similarity 100.0%; Pred. No. 8.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels
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SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
                  PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2010-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PELICATION NUMBER: PCT/USO1/00670
PRIOR PELICATION NUMBER: US 60/234,687
PRIOR PILING DATE: 2000-09-21
PRIOR PELICATION NUMBER: US 69/608,408
PRIOR PILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 69/608,408
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
APPLICATION NUMBER: PCT/US01/00663
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; ORGANISM: Homo sapiens
US-10-264-049-4044
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LENGTH: 97
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LENGTH: 168
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Sequence 169247, Application US/10437963

Sequence 169247, Application US/10437963

Sequence 169247, Application US/10437963

Publication No. US200640123343A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Cao, Yongwei

APPLICANT: Cao, Yongwei

APPLICANT: Barbazuk, Brad

APPLICANT: Burbazuk, Brad

APPLICANT: Burbazuk, Brad

APPLICANT: Li, Ping

TITLE OF INVENTION: Ping

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REPERBNCE: 38-21(5321)B

CURRENT FILLING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 169247

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; Publication No. US20040005579A1
; GENERAL INPORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFRENCE: PA133P1
; CURRENT APPLICATION NUMBER: US/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR FILING DATE: 2000-06-07
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US-10-437-963-169247
22 IQAVLSLYASGRITG 36
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SOFTWARE: Patentin Ver. 3.1
SEQ ID NO 3432
LENGTH: 183
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Best Local Similarity 100.
Matches 15; Conservative
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ORGANISM: Oryza sativa
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Gaps

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Sequence 282905, Application US/10424599;
Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Acou Yihua
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION UNDERS: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 282905
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PA137P1
CURRENT APPLICATION NUMBER: US/10/264,049
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: US/US01/18569
PRIOR APPLICATION NUMBER: US 60/209,467
PRIOR FILING DATE: 2001-06-07
PRIOR FILING DATE: 2000-06-07
PRIOR FILING DATE: 2000-06-07
STOR FILING DATE: 2000-06-07
STORY FILING DATE: 3000-06-07
STORY FILING DATE: 2010-06-07
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US-10-424-599-280810
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100.0%; Pred. No. 0.00019;
ive 0; Mismatches 0;
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100.0%; Pred. No. 0.00018;
tive 0; Mismatches 0;
                                                                                                                       NAME/KEY: unsure
LOCATION: (1)..(197)
OTHER INFORMATION: unsure at all Xaa locations
FRATURE:
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Publication No. US20040005579A1
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 15; Conservative
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Best Local Similarity 100.
Matches 15; Conservative
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US-10-264-049-4148
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                        LENGTH: 197
TYPE: PRT
ORGANISM: Glycine max
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US-10-424-599-282905
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  SEO ID NO 280810
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Sequence 280810, Application US/10424599

Publication No. US20040031072A1

SEQUENCEAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Toou Yihua

APPLICANT: Zhou Yihua

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

CURRENT APPLICANT: 2003-04-28

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684
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NOAMS/KEY: MISC FEATURE
NOAMS/KEY: (1747)
OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
                                                    INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
                                                                                                                               LOCATION: (22) —
OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
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Best Local Similarity 100.
Matches 15; Conservative
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                                                                                                                                                                                                             NAME/KEY: MISC_FEATURE LOCATION: (33)
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NAME/KEY: MISC FEATURE
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138 IQAVLSLYASGRITG 152
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ORGANISM: Glycine max
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ORGANISM: Glycine max
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Matches 15; Conserv
                                                                          US-10-424-599-206389
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LENGTH: 237
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                                                                                                   Query Match 100.0%; Score 71; DB 15; Length 208; Best Local Similarity 100.0%; Pred. No. 0.00019; Matches 15; Conservative 0; Mismatches 0; Indels (
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100.0%; Score 71; DB 16; Length 230;
Best Local Similarity 100.0%; Pred. No. 0.00021;
Matches 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                               Sequence 56, Application US/10002631C
Publication No. US20030157486A1
GENERAL INFORMATION:
APPLICANT: Graff, Jonathon M.
APPLICANT: Muenster, Matthew
TITLE OF INVENTION: METHODS TO IDENTIFY SIGNAL SEQUENCES;
FILE REPERENCE, A44943 090455.0243
CURRENT APPLICATION NUMBER: US/10/002,631C
CURRENT APPLICATION NUMBER: US/10/002,631C
CURRENT FILING DATE: 2001-10-31
NUMBER OF SEQ ID NOS: 324
SEQ ID NO 56
INDICTH: 219
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US-10-767-701-42770
                                               ; OTHER INFORMATION: Clone ID: PAT_MRT3847_97486C.l.pep
US-10-424-599-282905
LOCATION: (1)..(208)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
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US-10-002-631C-56
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1 IQAVLSLYASGRITG 15

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Sequence 206389, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: SON Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: 2003-04-28
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 206389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 14326, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5323)B
FILE REFERENCE: 38-21(5323)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
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US-10-424-599-143226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Clone ID: PAT_MRT3847_28396C.1.pep
US-10-424-599-206389
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100.0%; Pred. No. 0.00022;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (1)...(236)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KRY: unsure
NAME/KRY: unsure
(1)..(237)
OTHER INFORMATION: unsure at all Xaa locations
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Best Local Similarity 100.0
Matches 15; Conservative
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Gaps

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APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
PILE REPERRNCE: 38-21(5313) B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 44494
LENGTH: 250
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APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Screen, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Screen, Screen, Solate Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Screen, Jack E
APPLICANT: Screen, Jack E
APPLICANT: Screen, 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 71; DB 15;
100.0%; Pred. No. 0.00024;
tive 0; Mismatches 0;
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Pred. No. 0.00023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Clone ID: 700978095_FLI.pep
US-10-425-114-44494
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Best Local Similarity 100.0%;
Matches 15; Conservative 0
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hes 15; Conservative
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ORGANISM: Zea mays
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Publication No. US20040031072A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J

APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICANTON NUMBER: US/10/424,599
CURRENT APPLICANTON NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

LENGTH: 248
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Sequence 43575. Application US/10767701

Sequence 43575. Application US/2040172684A1

Sequence 43575. Application US/2040172684A1

GENERAL INFORMATION:

APPLICANT: Kovalic, David K.

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

TITLE OF INVENTION: Dlants and Uses Thereof For Plant Improvement

CURRENT APPLICATION NUMBER: US/10/767,701

CURRENT FILING DATE: 2004-01-29

SEQ ID NOS: 63128

LENGTH: 249
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100.0%; Score 71; DB 16; Length 249;
Best Local Similarity 100.0%; Pred. No. 0.00023;
Matches 15; Conservative 0; Mismatches 0; Indels
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US-10-767-701-43575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Clone ID: PAT_MRT3847_117922C.1.pep
US-10-424-599-162684
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; Sequence 44494, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
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ORGANISM: Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Glycine max
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Best Local S:
Matches 15
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Sequence 19404, A Sequence 11, Appl Sequence 4886, Ap Sequence 8829, Ap Sequence 8192, Ap Sequence 5362, Ap Sequence 5362, Ap Sequence 7396, Ap Sequence 7396, Ap Sequence 7396, Ap Sequence 7722, Ap

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Sequence 4, Appli Sequence 4, Appli Sequence 5, Appli Sequence 755, App Sequence 67, App

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Sequence:

Searched:

Database

Result

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APPLICANT: KIM, Dong Soo
APPLICANT: KIM, Chul Geun
APPLICANT: KIM, Chul Geun
APPLICANT: NAM, Yoon Kwon
APPLICANT: NAM, Yoon Kwon
APPLICANT: CHO, Kyou Nam
TITLE OF INVENTION: EXPRESSION VECTOR OF MUD LOACH GROWTH HORMONE GENE
FILE REPERBUCE: D063441050/BAS
CURRENT APPLICATION NUMBER: US/09/306,446C
CURRENT FILING DATE: 1999-05-06
PRIOR APPLICATION NUMBER: KR 98/20255
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 4
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US-08-609-236-6

i Sequence 6, Application US/08609236

j Patent No. 6087398

j TILLE OF INVENTION:

i TILLE OF INVENTION: No. 6087398el Sickle Cell Anemia Treatment

i WUMBER OF SEQUENCES:

c CORRESPONDENCE ADDRESS:

j ADDRESSEE: McGregor & Adler, LLP

STREET: 8011 Candle Lane

j STATE: Texas

COUNTRY: USA

ZIP: 77071

ZIP: 77071
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Pred. No. 4.8e-07;
             US-09-538-092-1109
US-09-248-796A-19404
US-09-114-001C-4962
US-09-107-532A-4886
US-09-107-532A-4886
US-09-543-681A-8292
US-09-949-011500
US-09-949-016-6655
US-09-949-016-7366
US-09-387-693-4
US-09-387-693-4
US-09-387-693-4
US-09-9132-210-755
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GENERAL INFORMATION:
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Best Local Similarity
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Sequence 731, App
Sequence 2, Appli
Sequence 6100, Ap
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6520, Ap
11110, Ap
6656, Ap
8452, Ap
395, App
12005, A
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                                                                                                                            // Search time 17.5333 Seconds
(without alignments)
63.863 Million cell updates/sec
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Sequence 5
Sequence 7
Sequence 7
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Sequence 6
Sequence 1
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/cgn2 6/ptodata/1/iaa/5B_COMB.pep:*
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/cgn2 6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2 6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2 6/ptodata/1/iaa/PCTUS_COMB.pep:*
               GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-08-106-217-16
US-09-106-217-16
US-09-949-016-6100
US-09-106-217-2
US-09-19-172-33
US-09-919-172-33
US-09-919-172-33
US-09-949-016-9424
US-09-949-016-11313
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US-09-171-337A-7
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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18-09-106-217-16
7 Sequence 16, Application US/09106217
7 Patent No. 6063576
                                                                                                                                                                                                                                                 Sequence 14, Application US/08494151 Patent No. 5840528
                                                                              1 DEAQSKRGILTLKYP 15
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amino acid
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TELEX: 90-4030
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                15; Conservative
                                                                                                                             56 DEAQSKRGILTLKYP
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                                   Matches
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APPLICANT: KIM, Dong Soo
APPLICANT: KIM, Dong Soo
APPLICANT: KIM, Chul Geun
APPLICANT: NOH, Jae Koo
APPLICANT: NOH, Jae Koo
INTITE OF INVENTION: EXPRESSION VECTOR OF MUD LOACH GROWTH HORMONE GENE
TITLE OF INVENTION: EXPRESSION VECTOR OF MUD LOACH GROWTH HORMONE GENE
TITLE OF INVENTION: EXPRESSION VECTOR OF MUD LOACH GROWTH HORMONE GENE
CURRENT APPLICATION NUMBER: US/09/306,446C
CURRENT APPLICATION NUMBER: KR 99/20255
PRIOR APPLICATION NUMBER: KR 99/20255
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
ILENGTH: 374
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100.0%; Pred. No. 2.6e-06;
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word for Macintosh
GURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/609,236
FILING DATE: March 1, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/002,288
FILING DATE: August 14, 1995
CLASSIFICATION: ATA:
APPLICATION NUMBER: 1995
CLASSIFICATION: 14, 1995
CLASSIFICATION: 1806
FILING DATE: August 14, 1995
CLASSIFICATION: INFORMATION:
FEBERRICE/DOCKET NUMBER: DS807
FELECOMMUNICATION INFORMATION:
TELEPHONE: 713-777-6908
FILIERAKY: 713-777-6908
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ORGANISM: Misgurnus mizolepus
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MOLECULE TYPE:
DESCRIPTION: Protein
HYPOTHETICAL: NO
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| INDIVIDUAL ISOLATE:
| DEVELOPMENTAL STAGE:
| TISSUE TYPE:
| CELL TYPE:
| CELL LINE:
| US-08-609-236-6
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Best Local Similarity
Matches 15; Conserva
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Best Local Similarity
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APPLICANT: Keating, Mark T.
APPLICANT: Clson, Timothy M.
TITLE OF INVENTION: Actin Mutations in Dilated
TITLE OF INVENTION: Cardiomyopathy, a Heritable Form of Heart Failure
UNDMERS OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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APPLICANT: Van Ooyen, Albert Johannes Joseph
TITLE OF INVENTION:
TITLE OF INVENTION:
TURBER OF SEQUENCES: 14
CORRESPONDENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 2000 Fernsylvania Ave. N.W., Suite 5500
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FOC-DOS/MS-DOS
SOFTWARE: PATEMIL Release #1.0, Version #1.25
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STREET: 555 Thirteenth Street, N.W., Suite 701 East
STREET: Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/494,151
FILING DATE: 23-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mureahige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 24615-20039.01
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPAX: (202) 887-0763
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100.0%; Score 76; DB 2; L
Best Local Similarity 100.0%; Pred. No. 2.6e-06;
Matches 15; Conservative 0; Mismatches 0;
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ZIP: 20004
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Sequence 6100, Application US/09949016

j Sequence 6100, Application US/09949016

j Retent No. 6812339

j GENERAL INFORMATION:
    TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WINDER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-00-03

PRIOR PILING DATE: 2000-00-03

PRIOR PILING DATE: 2000-00-03

SEQ ID NOS: 207012

SOFTWARE: FREESEQ for Windows Version 4.0

TENDORM. 3.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 376;
IITLE OF INVENTION: MALIGNANCY OF SMOOTH MUSCLE TUMORS
                                                                                                                                                                                                  COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMFUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/588,113
FILING DATE:
                     NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
ADDRESSEE: No. 5710003ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 76; DB 4; 100.0%; Pred. No. 2.6e-06; iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Ralph, Rebecca L.
REGISTRATION NUMBER: 35,152
REFREBUCE/DOCKET NUMBER: TJU-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DEAQSKRGILTLKYP 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 376 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0
Matches 15; Conservative
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Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , MOLECULE TYPE: protein US-08-588-113-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-949-016-6100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-949-016-6100
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                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
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Sequence 731, Application US/09976594
Patent No. 6673549
Fatent No. 6673549
GENERAL INFORMATION:
APPLICANT: Furness, Michael
APPLICANT: Buchbinder, Jenny
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
FILE REPRENCE: PA-0041 US
CURRENT APPLICATION NUMBER: US/09/976,594
CURRENT APPLICATION NUMBER: 60/240,409
PRIOR PILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 60/240,409
NUMBER OF SEQ ID NOS: 1143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                MEDIUM TYPE: FLOPPY disk
COMPUTER: 1BM PC compatible
COMPUTER: 1BM PC compatible
COMPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/106,217
FILING DATE:
CLASSIFICATION:
ATTONEY/AGENT INFORMATION:
NAME: Saxe, Stephen A.
REGISTRATION NUMBER: 38,609
REGISTRATION INFORMATION:
TELEPROMUNICATION INFORMATION:
TELEPRAK: 202-783-6031
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APPLICANT: MCHUGH, Kirk M.
TITLE OF INVENTION: DIAGNOSTIC TEST FOR DETERMINING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; FEATURE:
; NAME/KEY: misc_feature
; OTHER INCRMATION: Incyte ID No. 6673549 1837317CD1
US-09-976-594-731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 76; DB 3; I
Pred. No. 2.6e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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US-08-588-113-2
'Sequence 2, Application US/08588113
'Patent No. 5710003
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                                                                                                                                                                                                                                                                                                                                          TELEFAX: 202-783-6031
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DEAQSKRGILTLKYP 15
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Best Local Similarity 100.
Matches 15; Conservative
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MOLECULE TYPE: protein
US-09-106-217-16
  COMPUTER READABLE FORM:
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ORGANISM: Homo sapiens
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Matches 15; Conserv
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LENGTH: 375
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ORGANISM: Homo sapiens FEATURE:
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APPLICANT: Keating, Mark T.

APPLICANT: Olgen, Timothy M.

TITLE OF INVENTION: Actin Mutations in Dilated

TITLE OF INVENTION: Cardiomyopathy, a Heritable Form of Heart Failure
NUMBER OF INVENTION: 18

CORRESPONDENCE ADDRESS:
ADDRESSE: Rothwell, Figg, Ernst & Kurz, P.C.
STREET: 555 Thirteenth Street, N.W., Suite 701 Bast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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Pred. No. 2.6e-06;
Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                          CITY: Washington
STATE: DC
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/106,217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 33, Application US/09919172
Patent No. 6673545
GENERAL INFORMATION:
APPLICANT: Faris, Mary
TILLE OF INVENTION:
FILE REFERENCE: PA-0036 US
CURRENT APPLICATION NUMBER: US/09/919,172
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/222,469
PRIOR PILING DATE: 2000-07-28
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100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY AGENT INFORMATION:
NAME: Saxe, Stephen A.
REGISTRATION NUMBER: 38,609
REFRENCE/DOCKET NUMBER: 2323-
TELECOMUNICATION INFORMATION:
TELEPHONE: 202-783-6040
TELEPHONE: 202-783-6040
INFORMATION FOR SEC ID NO: 2:
                                                                                             US-09-106-217-2
; Sequence 2, Application US/09106217
; Patent No. 6063576
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 377 amino acida
TYPE: amino acid
57 DEAQSKRGILTLKYP
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Best Local Similarity 100.
Matches 15; Conservative
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MOLECULE TYPE: protein
US-09-106-217-2
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SOFTWARE: PERL Program
SEQ ID NO 33
LENGTH: 377
TYPE: PRT
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CLASSIFICATION:
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US-09-919-172-33
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Sequence 7721, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:
Patent No. 6812339

GENERAL INFORMATION:
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PILLING DATE: 2000-10-20
PRIOR FILLING DATE: 2000-10-03
PRIOR FILLING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012

SOUTH NOT 721

LENGTH: 386

LENGTH: 386
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GENERAL INFORMATION:

APPLICANT: Baak, Jan

TILE OF INVENTION: Prognostic Classification of Breast Cancer

FILE REFERENCE: B0801/724 (JRV)

CURRENT TILING DATE: 2001-07-27

FRICK APPLICATION NUMBER: US 60/222,093

FRICK APPLICATION NUMBER: US 60/222,093

FRICK FILING DATE: 2000-07-28

NUMBER OF SEQ ID NOS: 102

SOFTWARE: PatentIn version 3.0

SEQ ID NO 53

LENGTH: 377
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                                                                                 100.0%; Score 76; DB 4; Length 377; 100.0%; Pred. No. 2.6e-06; Ative 0; Mismatches 0; Indels
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NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673545 1709118CD1
US-09-919-172-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 76; DB 4; I Pred. No. 2.6e-06; ; Mismatches 0;
                                                                                                                                                                                                                                                                                           US-09-917-254-53; Sequence 53, Application US/09917254; Patent No. 6703204
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Best Local Similarity 100.0
Matches 15; Conservative
                                                                                                                              Conservative
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CRGANISM: Homo Sapiens
US-09-917-254-53
                                                                               Query Match
Best Local Similarity
Matches 15; Conserv
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Best Local Similarity
Matches 15; Conserv
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-949-016-7721
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Sequence 11313, Application US/09949016

Batent No. 681239
GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,756
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PLILING DATE: 2000-10-03
PRIOR PLILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 200-09-08
NUMBER OF SEQ ID NOS: 207012
SEQ ID NO 1313
SEQ ID NO 1313
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100.0%;
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Best Local Similarity 100.
Matches 15; Conservative
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                                              US-09-949-016-11313
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Sequence 9424, Application US/09949016

Sequence 9424, Application US/09949016

Sequence 9424, Application

Sequence 9424, Application

Sequence 9424, Application

Sequence 9424, Application

Sequence 942, Application

Sequence 042, Application

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## Sequence 10757, Application US/09949016

## Patent No. 6812339

## Patent No. 6812339

## Patent No. 6812339

## PAPLICANT: VENTER, J. Craig et al.

## TILLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

## TILLE OF INVENTION: WITH HUWAN DISEASE, METHODS OF DETECTION AND USES THEREOF

## CURRENT PAPLICATION NUMBER: 60/241, 755

## PRIOR PAPLICATION NUMBER: 60/241, 755

## PRIOR PAPLICATION NUMBER: 60/231, 468

## PRIOR PAPLICATION NUMBER: 60/231, 498

## PRIOR PAPLICATION NUMBER: 60/231, 498

## PRIOR PILING DATE: 2000-10-03

## PRIOR PILING DATE: 2000-03-04

## PRIOR PILING D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
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Pred. No. 2.8e-06;
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DEAQSKRGILTLKYP 15
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Best Local Similarity 100.
Matches 15; Conservative
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Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Human
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US-09-949-016-9424
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6/prodata/1/pubpaa/US09C_PUBCOMB.pep:*
6/prodata/1/pubpaa/US09 NEW PUB.pep:*
6/prodata/1/pubpaa/US10B_PUBCOMB.pep:*
6/prodata/1/pubpaa/US10B_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1418010 segs, 331997259 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DEAQSKRGILTLKYP 15
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Maximum DB seq length: 200000000
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76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Searched:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 3601, Ap	Sequence 37942, A	Sequence 47318, A	Sequence 280811,	Sequence 184471,	Sequence 280810,	Sequence 4308, Ap	Sequence 4148, Ap	Sequence 282905,	Sequence 56, Appl	Sequence 32056, A	Sequence 42770, A	Sequence 162684,
ΙD	US-10-264-049-3601	US-09-864-761-37942	US-10-767-701-47318	US-10-424-599-280811	US-10-424-599-184471	US-10-424-599-280810	US-10-264-049-4308	US-10-264-049-4148	US-10-424-599-282905	US-10-002-631C-56	US-10-029-386-32056	US-10-767-701-42770	US-10-424-599-162684
0.8	15	<u>ο</u>	16	15		15	15	15	15	14		16	15
% Duery Watch Length DB	105	108	135	136	142	197	201	204	208	219	219	230	248
% Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
Score	76	16	9/	9/	94	16	92	92	92	9/	92	9/	92
Result No.	-	7	٣	4	ß	9	7	80	0	10	11	12	13

14 76	100.0	331	15	US-10-425-114-59172	Sequence 59172, A
7	100.0	342	15	8-260A-400	4008
7	100.0	347	15	10-424-	
92 2	100.0	371	16	US-10-322-281-68	
7	100.0	375	14	-205 - 194 - 9	Sequence 93, Appl
7	100.0	375	14	.316-253-8	
7	100.0	375	15	ņ	
7	100.0	375	15	369-493-592	
7	100.0	375	15	-205-3	
7	100.0	375	15	-708-8	Sequence 82, Appl
7	100.0	376	15	US-10-341-434-101	
7	100.0	376	16	-437-963-202	
26 76	100.0	376		0-767-701-4567	45
7	100.0	377		US-09-919-172-33	33,
7	100.0	377	4	1-338-777-	e 52
7	100.0	377		US-10-236-031B-64	64
94 01	100.0	377	15	US-10-424-599-162009	Sequence 162009,
7	100.0	377		1-424-599-1	16
7	100.0	377		1-424-599-1	16
7	100.0	377		US-10-424-599-222816	Sequence 222816,
7	100.0	377		1-424-599-2	22349
	100.0	377	15	10-424-	N
92 9	100.0	377	15	10-425-114-6612	Sequence 66124, A
7	100.0	377	16	10-333-68	4
7	100.0	377	16	US-10-437-963-121952	٦
7	100.0	377	16	10-437-963-	1
40 76	100.0	377	16	10-437-963-1	e 1
7	100.0	377	16	-10-767-701-	e 47239,
7	100.0	378	12	-10-425-114-4231	e 4231
7	100.0	378	12	-10-425-114-5245	e 52458,
4 76	100.0	378	15	10-425-114-5	e 59265,
92 29	100.0	378	15	US-10-425-114-59967	Sequence 59967, A

ALIGNMENTS

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NAME/KEY: MISC_FEATURE

1 LOCATION: (103)

1 OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids

US-10-264-049-3601
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                                          Sequence 3601, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; CURRENT APPLICATION NUMBER: US/10/264,049
; CURRENT APPLICATION NUMBER: PCT/US01/18569
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR PILING DATE: 2001-06-07
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cch 100.0%; Score 76; DB 15; Length 105; al Similarity 100.0%; Pred. No. Se-06; 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
Matches 15; Conserva
RESULT 1
US-10-264-049-3601
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 3601
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RESULT 2

DEAQSKRGILTLKYP 71 1 DEAQSKRGILTLKYP 15

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us-09-423-351c-9.rapb

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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Solu Yihua
APPLICANT: Solu Yihua
APPLICANT: Can Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT FILEN DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 290811
                                                                                                                                                                                                                                                                                                                    APPLICANT: Zhou, Yihua APPLICANT: Zhou, Yihua APPLICANT: Zhou, Yihua APPLICANT: Cao, Yongwei TTLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement FILE REFERENCE: 38-21(53535)B CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 47318
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  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C105_2.pep
US-10-767-701-47318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Clone ID: PAT_MRT3847_95595C.1.pep
US-10-424-599-280811
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Pred. No. 6.7e-06;
; Mismatches 0;
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Pred. No. 6.6e-06;
; Mismatches 0;
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OTHER INFORMATION: unsure at all Xaa locations
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 280811, Application US/10424599 Publication No. US20040031072A1 GENERAL INFORMATION:
                                                                                                                                                                                                                       Sequence 47318, Application US/10767701 Publication No. US20040172684A1 GENERAL INFORMATION APPLICANT: Kovalic, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; So
Best Local Similarity 100.0%; Pi
Matches 15; Conservative 0;
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                                                1 DEAQSKRGILTLKYP 15
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                                                                                               15 DEAQSKRGILTLKYP 29
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ORGANISM: Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
  Conservative
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Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: unsure
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                                                                                                                                                                                                US-10-767-701-47318
     15;
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                                              PRICEAR NO. USGOODOOG49763A1
GENERAL INCORMATION:
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Chen, Wencheng
TITLE OF INVENTION: HARMA GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
TITLE OF INVENTION: GENE EXPESSION ANALYSIS BY MICROARRAY
TITLE OF INVENTION: GENE EXPESSION ANALYSIS BY MICROARRAY
CURRENT PAPLICATION NUMBER: US 001.05-23
PRIOR PELICATION NUMBER: US 001.05-23
PRIOR PELICATION NUMBER: US 001.05-24
PRIOR PELICATION NUMBER: US 001.05-24
PRIOR PELICATION NUMBER: US 001.05-26
PRIOR PELICATION NUMBER: US 001.05-26
PRIOR PELICATION NUMBER: US 00.05-26
PRIOR PELICATION NUMBER: PCT/USO1/0066
PRIOR PELING DATE: 2001-01-30
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HIT: 015998, EVALUE 9.00e-60
HIT: BF127509.1, EVALUE 2.00e-58
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N HERRY, SIGNAL = 62
N BONE MARROW, SIGNAL = 13
N LUNG, SIGNAL = 28
N PLACENTA, SIGNAL = 9.9
N ADULT LIVER, SIGNAL = 3.1
N FETAL LIVER, SIGNAL = 12
N BT474, SIGNAL = 27
N BRAIN, SIGNAL = 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HBL100, SIGNAL = 14
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SEQ ID NO 37942
                         Sequence 37942, Application US/09864761 Patent No. US20020048763A1
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SWISSPROT I
EST HUMAN I
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ORGANISM: Homo sapiens
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DEAGSKRGILTLKYP 72

58

Score 76; DB 9; Length 108; Pred. No. 5.2e-06;

100.0%;

Query Match Best Local Similarity

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73 DEAOSKRGILTLKYP 87
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NAME/KEY: MISC FEATURE
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                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: MISC FEATURE LOCATION: (145)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: MISC FEATURE LOCATION: (159)
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US-10-264-049-4148
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                                  Sequence 184471, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICANTON NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 184471
LENGTH: 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Willord: William of March 1992 1999 1 Sequence 280810, Application US/10424599  
Sequence 280810, Application US/204031072A1  
Sequence 280810, Application No. US2004031072A1  
Sequence 280810, Application No. US2004031072A1  
APPLICANT: La Rosa Thomas J  
APPLICANT: Lou Yihua  
APPLICANT: Zhou Yihua  
APPLICANT: Cao Yongwei  
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
FILE REFRENCE: 38-21(5.223)B  
CURRENT APPLICATION NUMBER: US/10/424,599  
CURRENT FILING DATE: 2003-04-28  
NUMBER OF SEQ ID NOS: 285684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 76; DB 15; Length 142; Pred. No. 7e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Clone ID: PAT_MRT3847_137594C.1.pep
US-10-424-599-184471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Clone ID: PAT_MRT3847_95594C.1.pep
US-10-424-599-280810
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LOCATION: (1)..(197)
OTHER INFORMATION: unsure at all Xaa locations
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; Sequence 4308, Application US/10264049
; Publication No. US20040005579A1
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Best Local Similarity 100.
Matches 15; Conservative
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Best Local Similarity 100.
Matches 15; Conservative
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RESULT 5
US-10-424-599-184471
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NAME/KEY: MISC FEATURE
LOCATION: (136)
OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
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LOCATION: (140)
OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
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1 LOCATION: (180)
2 OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-264-049-4308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
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APPLICANT: Birse et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PAI33P1
CURRENT APPLICATION NUMBER: US/10/264,049
CURRENT FILING DATE: 2002-10-04
FRIOR APPLICATION NUMBER: PCT/US01/18569
FRIOR APPLICATION NUMBER: PCT/US01/18569
FRIOR FILING DATE: 2001-06-07
FRIOR FILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 4360
SOFTWARE: Patentin Ver. 3.1
SEQ ID NO 4308
LENGTH: 201
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Sequence 32056, Application US/10029386
Publication No. US20030194704a1
Publication No. US20030194704a1
RUNDAMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GE.
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10S-10-767-701-42770
Sequence 42770, Application US/10767701
Sequence 42770, Application US/10767701
Sequence 42770, Application No. US20040172684A1
Sequence 42770, Application No. US20040172684A1
SEMENAL INFORMATION:
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REPRENCE: 38-21 (53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
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OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 16

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 23

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 6.8

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 20

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 9.8

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 9.8

OTHER INFORMATION: SWISSPROT HIT: P29751, EVALUE 3.00e-94
                                                                                                                                                                                                                                                                                                                                                   Query Match
100.0%; Score 76; DB 14;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 15; Conservative 0; Mismatches 0;
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  ; FILE REFERENCE: A34943 090495.0243;
; CURRENT APPLICATION NUMBER: US/10/002,631C;
; CURRENT APPLICATION NUMBER: 60/300,309;
; PRIOR APPLICATION NUMBER: 60/300,309;
; PRIOR FILING DATE: 2001-06-21;
; NUMBER OF SEQ ID NOS: 324;
; SOFTWARE: FastSEQ for Windows Version 4.0;
; SEQ ID NO 56;
; LENGTH: 219;
; VRQEANIEM: HOMO Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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Matches 15; Conserv
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LENGTH: 219
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APPLICANT: La Rosa Thomas J
APPLICANT: Rovalic David K
APPLICANT: Show Yibua
APPLICANT: About Yibua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 282905
LENGTH: 208
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0
                                                                            APPLICANT: Birse et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILER REFERENCE: PAINANTON: Nucleic Acids, Proteins, and Antibodies
FILER REFERENCE: PAINANTON: US/10/264.049
CURRENT APPLICATION NUMBER: US/10/264.049
PRIOR PILING DATE: 2002-10-04
PRIOR FILING DATE: 2001-06-07
PRIOR FILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 4360
SOFTWARE: Patentin Ver. 3.1
SEQ ID NO 4148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 76; DB 15; Length 204; 100.0%; Pred. No. 1e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 208;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Clone ID: PAT_MRT3847_97486C.1.pep
US-10-424-599-282905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 15; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: unsure
LOCATION: (1)..(208)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 282905, Application US/10424599; Publication No. US20040031072A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 10
US-10-002-631C-56
; Sequence 56, Application US/10002631C
; Publication No. US20030157486A1
; GENERAL INFORMATION:
; APPLICANT: Graff, Jonathon M.
appLICANT: Muenster, Matthew
Sequence 4148, Application US/10264049
Publication No. US20040005579A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 DEAQSKRGILTLKYP 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.
Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-049-4148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Glycine max
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Length 342;
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US-10-106-260A-4008
; Sequence 4008, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INPOWMATION:
    APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1e1 full length cDNA
; FILE REFERENCE: H1-A01.06
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT PILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                              0; Indels
                                              Score 76; DB 15;
Pred. No. 1.8e-05;
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                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: April 8, 2005, 12:51:00 Job time: 42.6667 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                100.0%;
                                                                                                                                               1 DEAQSKRGILTLKYP 15
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                                         Query Match
Best Local Similarity 100.0
Matches 15; Conservative
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Best Local Similarity 100.
Matches 15; Conservative
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US-10-108-260A-4008
US-10-425-114-59172
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Publication No. US20040034888A1

GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Deavid K.
APPLICANT: Application Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: NUMBER: US/10/425,114

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NO S-9172

LENGTH: 331
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US-10-424-599-162684
; Sequence 162684, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: La Rosa Thomas J
; APPLICANT: Zhou Yihua
; APPLICANT: Zhou Yihua
; APPLICANT: Cor Yongue
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Ass
; TITLE OF INVENTION: Blants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)8
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT APPLICATION NUMBER: US/10/424,599
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 162684
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                                                                                                                                                                                                                         Length 230;
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                                                                                                                                                                                                                  Query Match 100.0%; Score 76; DB 16; Length 2
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                          ; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C17410_1.pep
US-10-767-701-42770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Clone ID: PAT_MRT3847_117922C.1.pep
US-10-424-599-162684
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                                                                                                                                                                                                                                                                                                                                                  58 DEAQSKRGILTLKYP 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DEAQSKRGILTLKYP 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58 DEAOSKRGILTLKYP 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.04
Matches 15; Conservative
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 42770
LENGTH: 230
                                                                          TYPE: PRT
ORGANISM: Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Glycine max
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ORGANISM: Zea mays
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Gaps

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GenCore version 5.1.6
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OM protein - protein search, using sw model

April 8, 2005, 09:58:56; Search time 9.3333 Seconds (without alignments) 154.634 Million cell updates/sec Run on:

US-09-423-351C-8 75 1 LASLSTFQQMWISKQ 15 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 seqs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	actin alpha, smoot	actin - fruit fly	actin 5C - fruit f		actin CA15 - sea s	3 - fru	(clone	, fetal	- sea u	beta - b	1	æ	actin, aortic smoo		beta, c	actin beta - chick	beta - h	actin gamma 1 - hu		actin gamma - mous		σ	, cytosc	actin gamma - Emer	actin 1 - Pneumocy	모	- fissi		actin beta-1, cyto
SUMMARIES	ΩI		S14851	A28258	S39777	A61043	A03000	S11452	B25819	A29664	ATBOB	ATBOG	JC5818	ATBOSM	ATRIC	A48324	ATCHB	ATHUB	ATHUG	ATMSB	ATMSG	ATRBB	S11222	533386	JT0385	S47897	T25272	A26836	711	S71124
	BB	7	~	7	~	7	7	~	7	~	Н	Н	ď	-1	Н	Н	Н		-1	-	-	Н	Н	7	~	7	~	7	7	7
	Length	42	100	137	195	213	308	327	349	370	374	374	374	375	375	375	375	375	375	375	375	375	375	375	375	375	375	7	375	-
d	Query Match		100.0	100.0	100.0	100.0	100.0		100.0		٠.	-		•	100.0		100.0	٠.	٠.	٠.	100.0	100.0	100.0		100.0	100.0	100.0			100.0
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1 LASLSTFQQMWISKQ 15

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actin beta, cytoso	actin beta - goose	actin alpha, cardi	actin - Puccinia g	actin 7 - fruit fl	actin gamma, cytos	actin 8 - fruit fl	actin CyI - sea ur	Actin-1A - nematod	actin 87E - fruit	actin - fruit fly	actin, cytosolic -	actin, muscle - st	actin 15A - sea ur	actin - sea urchin	actin - Hydra atte
871126	A55001	A54728	S42103	ATFF7	A43552	ATFF8	ATURS	A48449	804538	JC1246	JS0189	JS0190	807288	809578	JQ0154
~	N	~	N	Н	н	Н	٦	~	N	N	C\$	~	~	N	N
375	375	375	375	376	376	376	376	376	376	376	376	376	376	376	376
100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
75	75	75	75	75	75	75	75	75	75	75	75	75	75	75	75
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS
 RESULT 1 JE0005 actin alpha, smooth muscle - rat (fragment) C;Species: Rattus norvegicus (Norway rat) C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004 C;Accession: JE0005
 R;Hsu, C.Y.J; Frankel, F.R. Gene 69, 345-348, 1988 Gene 69, 345-348, 1988 A;Title: Conserved and unique sequences in the 3'-untranslated region of rat smooth-musc A;Reference number: JE0005; MUID:89172079; PMID:3234770 A;Accession: JE0005
 A;Nolecule type: makna A;Residues: 1-42 <hsu3- A;Cross-references: UNIPROT:P70476; GB:M22757; NID:g949983; PIDN:AAA74457.1; PID:g695397 C;Genetics: A;Gene: mascie; actin C;Superfamily: actin C;Keywords: muscle; smooth muscle</hsu3-
Query Match 100.0%; Score 75; DB 2; Length 42; Best Local Similarity 100.0%; Pred. No. 2.3e-06; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 LASLSTFOOMWISKQ 15
RESULT 2 S14851 actin - fruit fly (Drosophila melanogaster) C;Species: Drosophila melanogaster C;Species: Drosophila melanogaster C;Date: 20-Peb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004 C;Accession: S14851
R;Burn, T.C.; Tobin, S.L. submitted to the EMBL Data Library, October 1990 A;Reference number: S14851 A;Accession: S14851 A:Molecule type: DNA
A;Residues: 1-100 <bur> A;Residues: 1-100 <bur> A;Cross-references: UNIPROT:P02572; EMBL:X54848; NID:g7549; PIDN:CAA38618.1; PID:g7550 C;Genetics: A;Genetics: A;Gene:FlyBase:Act42A A;Cross-references: FlyBase:FBqn0000043</bur></bur>
C;Superfamily: actin C;Keywords: cell motility; cytoskeleton; microfilament; mitosis; structural protein
Query Match 100.0%; Score 75; DB 2; Length 100; Best Local Similarity 100.0%; Pred. No. 5.6e-06; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Gaps

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RESULT 3

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A;Molecule type: DNA
A;Residues: 1-308 <FYR>.
A;Cross-references: UNIPROT:P02572
A;Note: there are 68 unsequenced residues between positions 160 and 161. Partial sequenc
A;Note: the authors translated the codon GTT for residue 263 as 11e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Accession: $11452
R;Macias, M.T.; Sastre, L.
Nucleic Acids Res. 18, 5219-5225, 1990
A;Title: Molecular cloning and expression of four actin isoforms during Artemia developm
A;Reference number: 'S11450; WUID:90384823; PMID:2402445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;MOLECULE type: mRNA
A;Residues: 1-327 <MAC>
A;Cross-references: UNIPROT:P18602; EMBL:X52604; NID:95666; PIDN:CAA36837.1; PID:9829162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cipate: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_cnauge varue. 2000.
CiAccession: A03000
RiFAS East Bond, B.J.; Hershey, N.D.; Mixter, K.S.; Davidson, N.
Cell 24, 107-116, 1981
Arritle: The actin genes of Drosophila: protein coding regions are highly conserved but A; Reference number: A03000; MUID:81210174; PMID:6263481
          A,Residues: 1-213 <BEA>
A,CTOSE references: UNIPROT:Q7M3Y7
A)CTOSE This sequence is expressed in cells undergoing rapid cell division.
C,Superfamily: actin
                                                                                                             C;Keywords: cytoskeleton; methylated amino acid; mitosis; structural protein F;73/Modified site: 3'-methylhistidine (His) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                           actin 3 - fruit fly (Drosophila melanogaster) (fragments)
C;Species: Drosophila melanogaster
C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        actin (clone 302) - brine shrimp (fragment)
C;Species: Artemia sp. (brine shrimp)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 75; DB 2; Length 308;
Pred. No. 1.7e-05;
; Mismatches 0; Indels
                                                                                                                                                                                      100.0%; Score 75; DB 2; Length 213; 100.0%; Pred. No. 1.2e-05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 75; DB 2; Length 327; 100.0%; Pred. No. 1.8e-05; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Keywords: methylated amino acid F;74/Modified site: 3'-methylhistidine (His) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Keywords: methylated amino acid; structural protein F;25/Modified site: 3'-methylhistidine (His) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.08;
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                                                                                                                                                                                   Query Match
Best Local Similarity 100.0
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100...
These 15; Conservative
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Best Local Similarity 100.0
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Map position: 42A
C; Superfamily: actin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Superfamily: actin
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R. Adamski, J.; Husen, B.; Thole, H.H.; Groeschel-Stewart, U.; Jungblut, P.W.
R. Adamski, J.; Husen, B.; Thole, H.H.; Groeschel-Stewart, U.; Jungblut, P.W.
B. Dicchem. J. 296, 797-802, 1993
A; Title: Linkage of 17-beta-oestradiol dehydrogenase to actin by epsilon-(gamma-glutamyl A; Reference number: S39777; MUID:94107247; PMID:8280079
A; Accession: S39777
A; MulD:94107247; PMID:8280079
A; Accession: S39777
A; Residues: 1-20,21-52;53-79;80-85;86-95;96-116;117-151;152-159;160-195 ADA>
C; Superfamily: actin
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A61043
actin CA15 - sea squirt (Styela clava) (fragments)
C;Species: Styela clava
C;Species: Styela clava
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: A61043
R;Bech, R.L.; Jeffery, W.R.
Dev. Genet. 11, 2-14, 1990
A;Title: Temporal and spatial expression of a cytoskeletal actin gene in the ascidian 8, Accession: A61043; MUID:90298580; PMID:2361333
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
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                                                                                                                                               actin 5C - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           actin beta - pig (fragments)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 07-Oct-1994 #sequence_revision 12-Apr-1996 #text_change 09-Jul-2004
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Pred. No. 1.1e-05;
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100.0%; Score 75; DB 2; I
Best Local Similarity 100.0%; Pred. No. 7.6e-06;
Matches 15; Conservative 0; Mismatches 0;
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Best Local Similarity 100.0%; P. Matches 15; Conservative 0;
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J. Biol. Chem. 258, 12153-12162, 1983
ArTitle: Regulation of protein synthesis in mitogen-activated bovine lymphocytes. Analy-A;Reference number: A39105; MUID:84032385; PMID:6195151
                                                                                                                                                                                                                                   A, Molecule type: mRNA
A, Residues: 76-227;334-374 < DEG>
A, Residues: 76-227;334-374 < DEG>
A, Cross-references: GB: K00622; BB: K00623
A, Note: actins beta and gamma were not distinguished in this study
C; Comment: Vertebrate nonmuscle cells contain two highly conserved cytoskeletal actins,
C; Superfamily: actin
C; Reywords: blocked amino end; cell motility; cytoskeleton; methylated amino acid; micr.
F; 1/Modified site: blocked amino end (Asp) (probably acetylated) #status experimental
F;72/Modified site: 3'-methylhistidine (His) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: B14185; A02999
R;Vandekerckhove, J.; Weber, K.
Eur. J. Biochem. 90, 451-462, 1978
A;Title: Actin amino-acid sequences. Comparison of actins from calf thymus, bovine brain A;Reference number: A14185; MUID:79045349; PMID:213279
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A)Cross-references: UNIPROT:P02571

A)Notes: only peptides that differed in composition from the corresponding peptides of r C;Comment: Vertebrate nonmuscle cells contain two highly conserved cytoskeletal actins, C;Superfamily: actin c;Superfamily: actin cell motility; cytoskeleton; methylated amino acid; micr: F;I/Modified site: blocked amino end (Glu) (probably acetylated) #status experimental F;I/Modified site: blocked amino end (Glu) (probably acetylated)
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C;Species: Homo sapiens (man)
C;Date: 20-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 09-Jul-2004
C;Date: 20-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 09-Jul-2004
C;Accession: JCS818; PC4501
R;Hauschildt, S.; Schwarz, C.; Heine, H.; Ulmer, A.J.; Flad, H.D.; Rietschel, E.T.; Jen Biochem. Biophys. Res. Commun. 241, 670-674, 1997
Biochem. Biophys. Res. Commun. 241, 670-674, 1997
A;Fitle: Actin: A target of lipopolysaccharid-induced phosphorylation in human monocyte A;Reference number: JC5818; MUID:98096379; PMID:9434766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Species: Bos primigenius taurus (cattle)
Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
Accession: B14185; A02999
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A;Residues: 1-61;84-112;147-190;196-209;215-253;335-358 <HA2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 75; DB 1; L
100.0%; Pred. No. 2.1e-05;
iive 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 2.1e-05;
Matches 15; Conservative 0; Mismatches 0;
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Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: protein A; Residues: 1-374 < HAU>
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                                                                                                                                                                                                                                                                                   C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 23-Aug-1887 #sequence_revision 23-Aug-1987 #text_change 09-Jul-2004
C;Date: 23-Aug-1887 #sequence_revision 23-Aug-1987 #text_change 09-Jul-2004
C;Accession: B25819
J. Mol. Evol. 23, 11-22, 1986
J. Mol. Evol. 23, 11-22, 1986
A;Title: Comparison of three actin-coding sequences in the mouse; evolutionary relations
A;Title: Comparison of three actin-coding sequences in the mouse; evolutionary relations
A;Title: Comparison of three actin-coding sequences in the mouse; evolutionary relations
A;Accession: B25819
A;Accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    actin - sea urchin (Strongylocentrotus purpuratus)
C;Species: Strongylocentrotus purpuratus (purple urchin)
C;Species: Strongylocentrotus purpuratus (purple urchin)
C;Species: Strongylocentrotus purpuratus (purple urchin)
C;Accession: A29664
R;Crain Jr., W.R.; Boshar, M.F.; Cooper, A.D.; Durica, D.S.; Nagy, A.; Steffen, D.
J. Mol. Evol. 25, 37-45, 1987
A;Title: The sequence of a sea urchin muscle actin gene suggests a gene conversion with A;Reference number: A29664, MUID:87311761; PMID:3114500
A;Accession: A29664
A;Moleule type: DNA
A;Residues: 1-370 <CRA>
A;CRA>
A;Cross-references: GB:X05739; GB:X05740; GB:X05741; GB:X05742; GB:X05743
A;Note: the authors translated the codon CAG for residue 260 as Glu
C;Keywords: methylated amino acid
F;73/Modified site: 3'-methylhistidine (His) #status predicted
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C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Date: 3.0-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: E14185; A39105; Ā02999; A14185
R;Vandekerckhove, J.; Weber, K.
Eur. J. Biochem. 90, 451-462, 1978
A;Title: Actin amino-acid sequences. Comparison of actins from calf thymus, bovine brain A;Reference number: A14185; MUID:79045349; PMID:213279
A;Accession: E14185
A;Molecule type: protein
A;Residues: 1-374 <VAN>
A;Molecule type: Drotein
A;Residues: 1-374 <VAN>
A;Coss-references: UNIPROT:P60712
A;Note: only peptides that differed in composition from the corresponding peptides of ra
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Pred. No. 2e-05;
Mismatches 0; Indels
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Pred. No. 2.1e-05;
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Best Local Similarity 100.0%; Pr
Matches 15; Conservative 0;
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Matches 15; Conservative
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A,Molecule type: DNA
A,Residues: 1-375 <LIU>
A,Cross-references: UNIPROT:P83750; GB:M24113; NID:g213041; PIDN:AAA68886.1; PID:g213042.
A,Note: the authors translated the codon TTC for residue 21 as Pro, AAG for residue 50 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C:Reywords: acetylated amino end; cell motility; cytoskeleton; methylated amino acid; mic; Reywords: acetylated amino end; cell motility; cytoskeletal #status predicted <wAT>
F;2-375/Product: actin beta, cytoskeletal #status predicted <wAT>
F;2/Modified site: acetylated amino end (Asp) (in mature form) #status predicted
F;73/Modified site: 3'-methylhistidine (His) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Note: the authors failed to translated the codon GGT for residue 42 as Gly
C;Comment: Vertebrate nonmuscle cells contain two highly conserved cytoskeletal actins,
                                                                                                                                                                                                                                                                                                                                                                                                             C, Accession: A48324
R;Liu, Z; Zhu, Z; Roberg, K.; Faras, A.; Guise, K.; Kapuscinski, A.R.; Hackett, P.B. DNA Seq. 1, 125-136, 1990
A;Title: Isolation and characterization of beta-actin gene of carp (Cyprinus carpio).
A;Reference number: A48324; MUID:92190540; PMID:2134183
                                                                                                                                                                                                                                                                                                                                           C;Species: Cyprinus carpio (common carp)
C;Date: 03-Feb-1994 #sequence_revision 11-Apr-1997 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 75; DB 1; Length 37
100.0%; Pred. No. 2.1e-05;
tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                      actin beta, cytoskeletal - common carp
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                                                                                                                                                  346 LASLSTFOOMWISKO 360
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Best Local Similarity
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                    15;
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A/Accession: A02997
A/Accession: A02997
A/Modified site: 340297; MUID:80047657; PMID:499690
A/Accession: A02997
A/Modified site: 31-36
A/Modified site: 3-methylhistidine dipopulos, A.E.
Biochim. Biophys. Acta 1091, 222-230, 1991
Biochim. Biophys. Acta 1091, 222-230, 1991
A/Title: Phosphorylase kinase from bovine stomach smooth muscle: a Ca(2+)-dependent prot A/Reference number: 813480
A/Accession: 813480
A/Accession: 813480
A/Accession: 813480
A/Residues: 40-49 < czEv.
A/Residues: 40-49 < czEv.
A/Residues: 40-49 czEv.
A/Residues: 40-49 czEv.
A/Rocie: this material appears to be actin of aortic smooth muscle type or a related mole C;Superfamily: actin
C;Keywords: acetylated amino end; methylated amino acid; muscle contraction
E/1/Modified site: acetylated amino end (Glu) #status predicted
F/1/Modified site: 3-methylhistidine (His) #status experimental
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C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Species: 13-0un-1983 #sequence_revision 13-0un-1983 #text_change 22-0un-1999
C;Accession: A38571; A02999
R;Nudel, U; Zakut, R; Shani, M.; Neuman, S.; Levy, Z.; Yaffe, D.
Nucleic Acids Res. 11, 1759-1771, 1983
A;Title: The nucleotide sequence of the rat cytoplasmic beta-actin gene.
A;Reference number: A38571; MUID:83168920; PMID:6300777
A;Residues: 1-375 ANDD
C;Goment: Vertebrate nonmuscle cells contain two highly conserved cytoskeletal actins, C;Genetics:
C;Goment: Vertebrate nonmuscle cells contain two highly conserved cytoskeletal actins, C;Genetics:
C;Goment: Vertebrate nonmuscle cells contain two highly conserved cytoskeletal actins, C;Genetics:
C;Goment: Vertebrate nonmuscle cells contain methylated amino acid; microfilament; mitosis; C;KSywords: cell motility; cytoskeleton; methylated amino acid; microfilament; mitosis; F;73/Modified site: 3'-methylhistidine (His) #status predicted
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ifferentiation 14, 123-133, 1979
!Title: The complete amino acid sequence of actins from bovine aorta, bovine heart,
C;Comment: This protein is involved in a signal transduction that eventually leads C;Superfamily: actin
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C;Species: Bos primingenius taurus (cattle)
C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 06-Sep-1996
C;Accession: A02997; S13480
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Pred. No. 2.1e-05;
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Pred. No. 2.1e-05;
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Best Local Similarity 100.0%; Pr
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Best Local Similarity 100.0%;
Matches 15; Conservative 0
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01-NOV-1997 (Rel. 35,
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TISSUE=Larva;
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01-NOV-1997
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132.739 Million cell updates/sec
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                                                                                       April 8, 2005, 09:58:56; Search time 57.8667 Seconds
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Q6j0r3
Q6j0r4
Q9ddz2
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Q90x51
Q9tyd9
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            GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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ACT3_LYTPI
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dictyocaulus viviparus (Bovine lungworm).
Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Strongylida,
Trichostrongyloidea, Dictyocaulidae, Dictyocaulinae, Dictyocaulus.
NCBI_TaxID=29172;
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Frosch M., Schnieder T.;
Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
    Q6jxi0
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Last annotation update)
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SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: Belongs to the actin family.
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Pfam; PF00022; Actin; 1.
PR0SITE; P800406; ACTINS_1; PARTIAL.
PROSITE; P800432; ACTINS_2; 1.
PROSITE; P801132; ACTINS_ACT_LIKE; PARTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                          Q6YMS6
ACT3 ARTSX
Q6BSW7
                                                                                                                                                     Q96WYS
Q96WY6
O35248
Q865W8
O18513
Q8WRE6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                            OGJX12
                                                                                                            Q6PJ43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR004001; Actin.
InterPro; IPR004000; Actin_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33 AA; 3830 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LASLSTFQQMWISKQ 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LASLSTFOOMWISKO 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U40590; AAA83551.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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1 LASLSTFQQMWISKQ 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 15; Conservative
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                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                          Actin 1.6 (Fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=6087;
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                                                                                                                                                      Q6J0R4
Q6J0R4;
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                                                                               RESULT 4
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"Nuclocide sequence of an actin-encoding gene from Hydra attenuata:
Btructural characteristics and evolutionary implications.";
Gene 84:55-64(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=201;
MEDLINE=90108717; PubMed=2606361; DOI=10.1016/0378-1119(89)90139-X;
                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
Parasitiformes; Ixodida; Ixodidae; Ixodes.
NCBI_TaxID=34613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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Hydridae; Hydra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
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                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
Rudenko N.K., Golovchenko M.P., Edwards M.J., Grubhoffer L.;
Rudenko N.K., Golovchenko M.P., Edwards M.J., Grubhoffer L.;
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY333957; AAG23081.1; -.
GO; GO:0005884; C:actin filament; IEA.
GO; GO:0005884; C:actin filament; IEA.
GO; GO:000509; F:structural constituent of cytoskeleton; IEA.
InterPro; IFR004001; Actin.
PROSITE; PS00432; ACTINS_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 75; DB 2; Length 38; 100.0%; Pred. No. 9.7e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38 AA; 4331 MW; D52EA0C57DC38864 CRC64;
                                                                      05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Gamma actin-like protein (Fragment).
Ixodes ricinus (Sheep tick)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 75; DB 2; I
100.0%; Pred. No. 1.2e-05;
iive 0; Mismatches 0;
38 AA
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Hydra attenuata (Hydra) (Hydra vulgaris)
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 LASLSTFOOMWISKO 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15; Conservative
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PRELIMINARY;
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Matches 15; Conserv
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Best Local Similarity
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SEQUENCE
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16 LASLSTFOOMWISKO 30

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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 24, Last annotation update)
Beta-actin (Fragment).
Micropterus salmoides (Largemouth bass).
Micropterus Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi,
Actinopterygii, Neopterygii, Teleostei; Euteleostei; Neoteleostei,
Acanthomorpha, Acanthopterygii; Percomorpha, Perciformes; Percoidei;
Centrarchidae; Micropterus.
                                                                                                                                                                                                                                                                                                               Fisher D.A., Bode H.R.; "Nucleotide sequence of an actin-encoding gene from Hydra attenuata: "Nucleotide sequence of an actin-encoding gene from Hydra attenuata: structural characteristics and evolutionary implications."; Gene 84:55-64(1989)
                                                                                                                                                                                                                                                                                       MEDLINE=90108717; PubMed=2606361; DOI=10.1016/0378-1119(89)90139-X;
                                                                                                                     Hydra attenuara (Hydra) (Hydra vulgaris).
Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;
Hydridae; Hydra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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EMBL; AX609159; AAT37544.1; -..

EMBL; AX609159; AAT37544.1; -..

GO; GO:0005200; Fisher filament; IEA.

GO; GO:0005200; Fisher on activity; IEA.

GO; GO:0005200; Fisher cural constituent of cytoskeleton; IEA.

InterPro; IPR004001; Actin.

PROSITE; PS00432; ACTINS_2; 1.

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SEQÜENCE 45 AA; 5159 MW; 7796EDEF78D574D0 CRC64;
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GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
InterPro; IPR004000; Actin_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 75; DB 2; Length 45; 100.0%; Pred. No. 1.2e-05;
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                                       05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
45 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50 AA.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Actinopterygii, Neopterygii, Teleostei, Buteleostei, Neoteleostei, Acanthomorpha, Acanthopterygii, Percomorpha, Atherinomorpha; Cyprinodontiformes, Fundulidae, Fundulus.
                                                                                                                                                                                                                                                                                                                                                                                                 Anas platyrhynchos (Domestic duck).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO; GO:0005884; C:actin filament; IEA.
GO; GO:0003774; F:motor activity; IEA.
GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
                                                         Score 75; DB 2; Length 56; Pred. No. 1.4e-05; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 75; DB 2; Length 93;
Pred. No. 2.4e-05;
; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Liver;
Roling J.A., Baldwin W.S.;
Submirted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF4550922; AAL29465.1; -.
HSSP; P02568; 1025.
GO; GO:0005884; C:actin filament; IEA.
GO; GO:0003774; P:motor activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIŠSUE-Spleen;
Sreekumar E., Premraj A., Rasool T.J.;
Submitrcd (MAR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY251275; AAP04479.1; --
HSSP; P02568; 1QZ5.
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  1 1
56 AA; 6339 MW; 3532A4205AC550E5 CRC64;
                                                                                                                                                                                                                                                                                                                                       01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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InterPro; IPR004000; Actin like.
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PROSITE; PS00432; ACTINS_2; 1.
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                                                                                                                                                1 LASLSTFQQMWISKQ 15
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                                                           Query Match 100.
Best Local Similarity 100.
Matches 15, Conservative
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Best Local Similarity 100.
Matches 15; Conservative
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Cynops pyrrhogaster (Japanese common newt).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae; Cynops.
NCBI_TaxID=8330;
                                                                                                                                                                                                                                                                                                                                   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Beta-actin (Fragment).
Borocrhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Bukaryota, Metazca; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Buteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
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Schwindt A.R., Alonso M., Leong J.C., Schreck C.B.;
Schwindt A.R., Alonso M., Leong J.C., Schreck C.B.;
Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AFS5083; AAN74801.1;
HSSP; P02568; 1MA9;
GO; GO:0015629; C:actin cytoskeleton; IEA.
GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
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Mizuno M., Takabatake T., Takahashi T.C., Takeshima K.;

Mizuno M., Takabatake T., Takahashi T.C., Takeshima K.;

"pax-6 gene expression in newt eye development.";

Dev. Genes Evol. 207:167-176 (1997).

EMBL; D64017; BAA24031.1; -.

EMBL; D6268; LLCU.

G0; G0:0003774; F:motor activity; IEA.

G0; G0:0003774; F:motor activity; IEA.

G0; G0:000500; F:seructural constituent of cytoskeleton; IEA.

InterPro; IPR004000; Actin_like.
                   Length 50;
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55 AA; 6163 MW; 9A4319FB34DD79D8 CRC64;
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(TrEMBLrel. 23, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
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057575;
01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                   100.0%; Score 75; DB 2; I
100.0%; Pred. No. 1.3e-05;
Live 0; Mismatches 0;
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                                                                                                   1 LASLSTFOOMWISKO 15
                                                                                                                                           35 LASLSTFOOMWISKO 49
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Best Local Similarity 100...
Best Local Similarity 100...
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nes 15; Conservative
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Matches 15;
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Sparidae; Pagrus.
NCBI_TaxID=143350;
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QGUIS1
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Sciuridae, Sciurinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-92249656; PubMed=1577198;
Beach K.., Jeffery W.R.;
Beach K.., Jeffery W.R.;
"Multiple actin ges encoding the same alpha-muscle isoform are expressed during ascidian development.";
Dev. Blol. 151:55-66(1992).
EMBL; L13788; AAA29846.1; --
HSSP; P02568; 1QZ5.
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MEDLINE-22554704; PubMed=12668969; DOI=10.1053/jhep.2003.50154;
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GO; GO:0003774; F:motor activity; IEA.
GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
GO; GO:0005200; F:structural constituent of cytoskeleton; IEA. Pfam; PF00022; Actin; 1. PROSITE; PS00432; ACTINS_2; 1.
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                                                                                                                                                                       Score 75; DB 2; Length 96;
Pred. No. 2.5e-05;
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100.0%; Pred. No. 2.6e-05; ....marches 0; Indels
                                                                                                                                                                                                                      0; Indels
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Bukaryota, Metazoa, Chordata, Urochordata, Ascidiacea,
Stolidobranchia, Styelidae, Styela.
NCBI_TaxID=7725;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100 AA; 11264 MW; 108CE34548BABB5E CRC64;
                                                                                                                        96 AA; 10798 MW; 7440DA6AE5A070C4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -MAY-2000 (TrEMBLrel. 13, Created)
-MAY-2000 (TrEMBLrel. 13, Last sequence update)
-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Beta-actin (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                       100 AA.
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100.0%; Pre
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InterPro; IPR004000; Actin_like.
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PROSITE; PS00432; ACTINS_2; 1.
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                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 15, Conservative
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Best Local Similarity 100.0
Matches 15, Conservative
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05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
15-UUL-2004 (TrEMBLRel. 27, Last an
Wang Y., Menne S., Jacob J.R., Tennant B.C., Gerin J.L., Cote P.J.;
"Role of type 1 versus type 2 immune responses in liver during the onset of chronic woodchuck hepatitis virus infection.";
Hepatology 37:771-780(2003).
HEBL; AY170121; AA0339434.1; -.
HSSP; P10983; 1D4X.
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GOS GO: 000584; C:actin filament; IEA.

GO; GO: 0003774; F:motor activity; IEA.

GO; GO: 0005200; F:structural constituent of cytoskeleton; IEA.

InterPro; IPR004001; Actin.

InterPro; IPR004000; Actin_like.
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Chen S.L., Xu M.Y., Hu S.L., Li L.;
"Analysis of immune-relevant genes expressed in red sea bream
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aquaculture 240:115-130(2004).

EMBL, AX190676; AAR20152.1; -.

GO: GO:000584; C:actin filament; IEA.

GO: GO:0005774; F:mctor activity; IEA.

GO: GO:0005200; F:structural constituent of cytoskeleton; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 75; DB 2; Length 106; 100.0%; Pred. No. 2.8e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE 106 AA; 11864 MW; 9FFDC145651FE343 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00022; Actin; 1.
PROSITE; PS00432; ACTINS_2; 1.
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PROSTITE; PS00432; ACTINS_2; 1.
NON TER 1 1 1 1 SEQUENCE 113 AA; 12550 MW;
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Best Local Similarity 100.000
Best Local 15, Conservative
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Les 15; Conservative
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Macaca mulatta (Rhesus macaque)

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95 LASLSTFOOMWISKO 109
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                                                                                                                                                                  MEDLINE=22946167; PubMed=14557539; DOI=10.1073/pnas.2135499100; Caceres M., Lachuer J., Zapala M.A., Redmond J.C., Kudo L., Caceres M., Lachuer J., Zapala M.A., Redmond J.C., Kudo L., Caceres M., Lockhart D.J., Preuss T.M., Barlow C.; Eschwarted gene expression levels distinguish human from non-human primate brains."; Proc. Natl. Acad. Sci. U.S.A. 100:13030-13035(2003).

EMBL; AR369786; AAR11223.1; Gliament; IEA.

GO; GO:0005884; C:actin filament; IEA.

GO; GO:0005774; F:motor activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

MEDLINE=22946167; PubMed=14557539; DOI=10.1073/pnas.2135499100;
Caccarán w. Lachuer J., Zapala M.A., Redmond J.C., Kudo L.,
Geschwind D.H., Lockhart D.J., Preuss T.M., Barlow C.;
Flevated gene expression levels distinguish human from non-human primate brains.";
Proc. Natl. Acas. Sci. U.S.A. 100:13030-13035(2003).

BEML; AY369785; AAR11222.1; -..
GO; GO:0005884; P:motor activity; IEA.
GO; GO:0005700; F:structural constituent of cytoskeleton; IEA.
                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Pan.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123 AA; 13874 MW; BB0A1DA9C05599E1 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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InterPro; IPR004000; Actin_like.
SMART; SM00268; ACTIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR004001; Actin.
InterPro; IPR004000; Actin_like.
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Matches 15; Conservative
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                                                                        Cercopithecinae; Macaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                  NCBI_TaxID=9544;
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SEQUENCE
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AC 060118
DT 05-70
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8, 2005, 12:03:11

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01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
Skeletal alpha-actin (Fragment).
Gillichthys mirabilis (Long-jawed mudsucker).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Acanthomorpha; Acanthopterygii; Teleostei; Buteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Gobioidei;
NCBI TaxID=8222;
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                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

TISSUE-Skeletal white muscle;

MEDLINE-21117151; PubMed=11172064; DOI=10.1073/pnas.98.4.1993;

Gracey A.Y., Troll J.V., Somero G.N.;

"Hypoxia-induced gene expression profiling in the euryoxic fish
gillichthys mirabilis.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0015629; C:actin cytoskeleton; IEA.
GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
InterPro; IPR004000; Actin_like.
Pfam; PF00022, Actin_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 75; DB 2; Length 124;
Pred. No. 3.2e-05;
Mismatches 0; Indels
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EMBL; AF266232; AAG13352.1; -.
HSSP; P02568; 1Q25.
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

8, 2005, 09:58:56 ; Search time 62.4 Seconds April Run on:

(without alignments) 92.971 Million cell updates/sec

US-09-423-351C-9 76 1 DEAQSKRGILTLKYP 15 score: Title: Perfect 6

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 seqs, 386760381 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2000s:* geneseqp2001s:* geneseqp2002s:* A_Geneseq_16Dec04:* geneseqp1980s:* geneseqp1990s:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:*

SUMMARIES

Result		* Query					
No.	Score	Match	Length	四	ΙD	Description	E
ч	76		15		AAW92535	Aaw92535	Beta-act
~	9/	100.0	54	•	AAG18905	Aag18905	Zea maye
m	16	100.0	58		AAG18945	Aag18945	Zea maye
4	16	100.0	73	•	AAG27057	Aag27057	Zea maye
Ŋ	16	100.0	74	•	AAG18936	Aag18936	Zea mays
9	16	100.0	75	ო	AAG18944	Aag18944	Zea maye
7	16	100.0	79		AAG12594	Aag12594	
8	92	100.0	82		AAG18904	Aag18904	Zea mays
σ	16	100.0	88	•	AAG18916	Aag18916	Zea may
10	9/	100.0	91		AAG18935	Aag18935	Zea mays
11	92		95	m	AAG19142	Aag19142	Zea maye
12	9/	100.0	96	ო	AAG12593	Aag12593	Zea may
13	9/	100.0	66	ო	AAG18903		Zea may
14	16	100.0	101	m	AAG27056		Zea mays
15	16		105	Ŋ	ABP42469	σ	Human ov
16	16	100.0	108	4	AAM18324	₩.	Peptide
11	16	100.0	108	4	ABB37358	Abb37358	Peptide
18	16	100.0	108	4	AAM30812	Aam30812	Peptide
19	16	100.0	108	4	ABB32106	Abb32106	Peptide
20	16	100.0	108	4	ABB22644	Abb22644	Protein
21	16	100.0	108	4	AAM70488	Aam70488	Human bo
22	16	100.0	108	4	AAM58048	_	Human b
23	16	100.0	108	4	ABG52170	Abg52170	Human 1
24	16	100.0	0	4	AAM05932	Aam05932	Peptide
25	9/	100.0	108	'n	ABG40127	Abg40127	Human pe

Aag19141 Zea mays Aag1815 Zea mays Aag1814 Zea mays Aag1814 Zea mays Abg15101 Novel hum Abg26865 Novel hum Abg26869 Novel hum Aau33077 Novel hum Abg43176 Human ova Abm73899 DNA clone Abc58422 Human gen Abg50847 Arabidops Aag50947 Arabidops Aag50947 Arabidops Aag5015 Arabidops Aag50115 Arabidops Aag50511 Arabidops Aag37210 Arabidops Aag50514 Arabidops	-
AAG19141 AAG18915 AAG18914 AAG18914 ABG18914 ABG18914 ABG6869 AAG3107 ABA43107 ABA73899 ABA73899 ABA73899 ABA73899 ABA73899 ABA73899 AAG00383 AAG00115 AAG05114	AAG37209
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## ALIGNMENTS

RESULT 1

Peptide substrate; CCT; eukaryotic type II chaperonin complex; cyclin; binding agent; substrate-binding site; SBS; substrate folding; actin; tubulin; treatment; cancer; anticancer drug; viral infection; screening; reduced toxicity. Beta-actin reference peptide substrate #9. AAW92535 standard; peptide; 15 AA (first entry) 26-APR-1999 AAW92535; AAW92535 

WO9853322-A1 Synthetic.

26-NOV-1998.

98WO-GB001485. 97GB-00010762. 22-MAY-1998; 23-MAY-1997; (CANC-) INST CANCER RES ROYAL CANCER HOSPITAL.

Liou AK; Hynes G, Willison K,

WPI; 1999-070162/06.

Identifying specific binding agents for substrate binding site in CCT chaperonin complex - also new peptide binding agents and their mimetics, and peptides containing a specific CCT binding site, used for treating

Disclosure, Fig 10; 97pp; English.

This invention describes a method which uses the CCT (eukaryotic type II chaperonin) complex or part of it, for identifying a binding agent that can occupy a substrace-binding site (SBS) on the CCT complex. By binding act to the CCT complex, the binding agents block an SBS so that biological activity of the CCT complex is affected, particularly its ability to fold substrates such as actin, tubulin and cyclin. The binding agents are useful for treatment of cancer, particularly when used in combination with an anticancer drug, or viral infections. Nucleic acid fragments are used to screen for agents, e.g. binding agents that modulate interaction between the CCT complex and a protein that is to be folded. The binding

# Yan

us-09-423-351c-9.rag

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990S-0137528P.
990S-0137528P.
990S-0137528P.
990S-013864P.
990S-0139163P.
990S-0139163P.
990S-0139453P.
990S-014085P.
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990S-014333P.
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990S-0145089P.
990S-0145089P.
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                    909
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agents may target cells that are actively synthesising tubulin etc. (unlike known microtubule-stabilising agents that affect all cells) should have reduced toxicity for normal cells. AAW92527-W92541 are peptide substrates used in the method of the invention
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9908-01314219P

9908-0134219P

9908-0134219P

9908-0134219P

9908-0134218P

9908-013452P

9908-0136782P

9908-0136782P

9908-0137508P

9908-0139452P

9908-0139452P

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9908-0139452P

9908-0139452P

9908-0139452P

9908-0139452P

9908-0139452P
25-FEB-2000; 2000EP-00301439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
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18-JUN-1999;
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AAG18936 standard; protein; 74 AA.

AAG18936;

27

13

g

RESULT 5 AAG18936

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PR 18—UW-1999 9918-013975.0P.

PR 21—UW-1999 9918-013975.0P.

PR 22—UW-1999 9918-013976.P.

PR 22—UW-1999 9918-013976.P.

PR 23—UW-1999 9918-013976.P.

PR 23—UW-1999 9918-013978.P.

PR 01—UU-1999 9918-01428.P.

PR 02—UU-1999 9918-01428.P.

PR 12—UW-1999 9918-01462.P.

PR 12—UW-1999 9918-01463.P.

PR 12—UW-1999 9918-01463.P.

PR 12—UW-1999 9918-01463.P.

PR 20—UW-1999 9918-01493.P.

PR 20—UW
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        red. No. 4.5e-06;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 76; DB
Pred. No. 4.5e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zea mays protein fragment SEQ ID NO: 20554.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAG18944 standard; protein; 75 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
       9905-0151066P

9905-0151030P

9905-0151303P

9905-0151330P

9905-015233P

9905-015313P

9905-0154019P

9905-0154039P

9905-0154139P

9905-0154139P

9905-0154139P

9905-0155139P

9905-0155139P

9905-015629P

9905-015923P

9905-01604P

9905-01604P

9905-01604P

9905-01609B

9905-01609B
                                                                                                                                                                                                                                                                                                                                                                                                                        990S-0161361P.
990S-0161920P.
990S-0161992P.
990S-0161993P.
990S-0162142P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
99US-0151065P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEAQSKRGILTLKYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
es 15; Conserv
        27-AUG-1999;
27-AUG-1999;
31-AUG-1999;
01-SEP-1999;
07-SEP-1999;
10-SEP-1999;
11-SEP-1999;
11-SEP-1999;
11-SEP-1999;
20-SEP-1999;
                                                                                                                           24-SEP-1999;
28-SEP-1999;
04-0CT-1999;
05-0CT-1999;
06-0CT-1999;
13-0CT-1999;
13-0CT-1999;
13-0CT-1999;
14-0CT-1999;
14-0CT-1999;
14-0CT-1999;
14-0CT-1999;
14-0CT-1999;
14-0CT-1999;
                                                                                                                                                                                                                                                                                                                                                  22-0CT-1999;
22-0CT-1999;
22-0CT-1999;
25-0CT-1999;
25-0CT-1999;
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26-OCT-1999;
28-OCT-1999;
28-OCT-1999;
28-OCT-1999;
                                                                                                          22-SEP-1999
                                                                                                                   23-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Si
Matches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAG18944;
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9905-0141287P

9905-0141287P

9905-01421842P

9905-0142390P

9905-014230P

9905-014230P

9905-014290P

9905-014290P

9905-014290P

9905-0142917P

9905-0142917P

9905-0143312P

9905-0144332P

9905-0149332P

9905-014933P

9905-014933P

9905-014932P

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9905-014932P

9905-014933P

9905-014933P

9905-014933P

9905-015066P

9905-0151066P
                                                                                                                                                                                                                                                                                                                                                        02-AUG-1999
02-AUG-1999
04-AUG-1999
04-AUG-1999
05-AUG-1999
06-AUG-1999
06-AUG-1999
10-AUG-1999
11-AUG-1999
11-AUG-1999
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11-AUG-1999
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11-AUG-1999
12-AUG-1999
21-AUG-1999
                                                                                                                                                                                                                                                                                                                                        -JUL-1999;
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07-SEP-1999;
                                                                                    9905-0121825P

9905-0123180P

9905-012548P

9905-0126788P

9905-0126788P

9905-0126788P

9905-0126788P

9905-012678P

9905-012874P

9905-0130891P

9905-0132448P

9905-0132448P

9905-0132448P

9905-013248P

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9905-013248P

9905-013248P

9905-013248P

9905-013248P

9905-013248P

9905-0134421B

9905-013442P

9905-013442P

9905-013442P

9905-013442P

9905-013442P

9905-013442P

9905-013442P

9905-013444P

9905-013442P

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9905-013444P

9905-0134452P

9905-0139458P

9905-0139458P

9905-0139458P

9905-0139458P

9905-0139458P

9905-0139458P

9905-0139463P

9905-0139463P

9905-0139463P

9905-0139463P
                                                                     2000EP-00301439
termination sequence; corn.
                Zea mays subsp. mays
                                                                                                                                                                                                                                                                                                                                        19 MXY - 1999
20 MAY - 1999
24 MAY - 1999
25 MAY - 1999
26 MAY - 1999
27 - MAY - 1999
33 - 70N - 1999
04 - 70N - 1999
06 - 70N - 1999
10 - 70N - 1999
10 - 70N - 1999
10 - 70N - 1999
                                                                     25-FEB-2000;
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16-JUN-1999;
16-JUN-1999;
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18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
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18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
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23-JUN-1999;
24-JUN-1999;
                                  EP1033405-A2
                                                   06-SEP-2000
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9905-01231809-9905-01235489-9905-01235489-9905-01262649-9905-01262649-9905-01262649-9905-01262649-9905-01262649-9905-01306499-9905-01306499-9905-01306499-9905-01306499-9905-01306499-9905-01306919-9905-01342689-9905-01342689-9905-01342689-9905-01342689-9905-01342689-9905-0134269-9905-0139459-9905-01394599-9905-01394609-9905-01394609-9905-01394609-9905-01394609-9905-01394609-9905-01394609-9905-01394619-9905-01394619-9905-01394619-9905-01394619-9905-01394619-9905-01394619-9905-01394619-9905-01394619-9905-0140929-9905-0140929-9905-01418429-9905-01418429-9905-01418429-9905-01418429-9905-01418429-9905-01418429-9905-01418429-9905-01418429-9905-01418429-9905-01418429-9905-01418429-9905-01418429-9905-01418429-9905-01418429-9905-01423909-
          25-FEB-2000; 2000EP-00301439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUL-1999;
02-JUL-1999;
06-JUL-1999;
                                                                                                                                                                                                                       06-MAY-1999
                                                                                                                                                                                                                                                              14-MAY-1999,
14-MAY-1999,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-JUN-1999
18-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-JUN-1999
                                                                                                                                                                                                             05-MAY-1999
                                                                                                                                                                                                                                                     11-MAY-1999
                                                                                                                                                                                                                                                                                 4-MAY-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8-JUN-1999
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                                                                                                                                                                                                                                                                                                                         20-MAY-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence; corn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 3; L
4.5e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zea mays protein fragment SEQ ID NO: 11768.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 76;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAG12594 standard; protein; 79 AA
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        990S-0153758P

990S-015473P

990S-015473P

990S-015513P

990S-015565P

990S-015565P

990S-015565P

990S-015713P

990S-015723P

990S-015723P

990S-015823P

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990S-01609BP

990S-016135P

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990S-016135P

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990S-016135P

990S-016135P

990S-016135P

990S-016135P
                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
99US-0153070P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEAQSKRGILTLKYP 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zea mays subsp. mays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 15; Conserv
        13-SEP-1999
16-SEP-1999
20-SEP-1999
21-SEP-1999
22-SEP-1999
24-SEP-1999
24-SEP-1999
06-0CT-1999
06-0CT-1999
13-0CT-1999
13-0CT-1999
14-0CT-1999
12-0CT-1999
12-0CT-1999
13-0CT-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58
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PR 08-JUL-1999 9 99US-0142320P.
PR 13-JUL-1999 9 99US-0142377P.
PR 14-JUL-1999 9 99US-0142377P.
PR 14-JUL-1999 9 99US-0143624P.
PR 15-JUL-1999 9 99US-0144036P.
PR 15-JUL-1999 9 99US-0144036P.
PR 19-JUL-1999 9 99US-0144036P.
PR 19-JUL-1999 9 99US-0144332P.
PR 19-JUL-1999 9 99US-0144332P.
PR 19-JUL-1999 9 99US-0144332P.
PR 21-JUL-1999 9 99US-0144332P.
PR 22-JUL-1999 9 99US-014532P.
PR 13-JUC-1999 9 99US-014332P.
PR 23-JUC-1999 9 99US-0143332P.
PR 23-JUC-1999 9 99US-014332P.
PR 23-JUC-1999 9 99US-0143332P.
PR 23-JUC-1999 9 99US-014332P.
PR 23-JUC-1999 9 99US-014332P.
PR 23-JUC-1999 9 99US-014332P.
PR 23-JUC-1999 9 99US-014332P.
PR 23-J
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence; corn.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Score 76; DB 3; Length 79;
; Pred. No. 4.8e-06;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zea mays protein fragment SEQ ID NO: 20498.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0121825P.
99US-0123180P.
99US-0123548P.
99US-0125788P.
990S-0155659P.
990S-0156488P.
990S-0156783P.
990S-0157117P.
990S-0157713P.
990S-0158029P.
990S-015823P.
990S-015823P.
990S-015923P.
990S-015923P.
990S-015933P.
990S-015933P.
990S-015933P.
990S-015933P.
990S-01609BP.
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ilarity 100.0%;
Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zea mays subsp. mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-FEB-1999;
05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
  24-SEP-1999;
28-SEP-1999;
04-0CT-1999;
05-0CT-1999;
06-0CT-1999;
07-0CT-1999;
13-0CT-1999;
13-0CT-1999;
14-0CT-1999;
14-0CT-1999;
14-0CT-1999;
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14-0CT-1999;
12-0CT-1999;
21-0CT-1999;
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22-0CT-1999;
23-0CT-1999;
23-0CT-1999;
24-0CT-1999;
25-0CT-1999;
25-0CT-1999;
26-0CT-1999;
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Matches
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AAG18904
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9905-0126785P

9905-0126785P

9905-0126785P

9905-0128714P

9905-0128714P

9905-0130843P

9905-0130843P

9905-01318449P

9905-0131848P

9905-0131848P

9905-0132481P

9905-0132481P

9905-0132481P

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9905-0132481P

9905-0132481P

9905-013421B

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9905-013421P

9905-013465P

9905-0139463P

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9905-014063P

9905-014063P

9905-014284P

9905-014284P

9905-014284P

9905-014284P

9905-014284P

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9905-014284P

9905-014284P

9905-014284P
                                                                                                                                                                                                                                                                                            02-JUL-1999;
06-JUL-1999;
08-JUL-1999;
09-JUL-1999;
12-JUL-1999;
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15-JUL-1999;
16-JUL-1999;
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07-JUN-1999;
08-JUN-1999;
10-JUN-1999;
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16-JUL-1999	99US-0144313E
19-UUL-1999	99US-014431E
19-UUL-1999	99US-014431E
19-UUL-1999	99US-014431E
19-UUL-1999	99US-014431E
19-UUL-1999	99US-014501E
19-UUL-1999	99US-014301E
19-UUL-1999	99US-01

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990S-0130449P

990S-0130510P

990S-0131449P

990S-013248BP

990S-0134221P

990S-0134221P

990S-013422P

990S-013452P

990S-0139452P

990S-0139452P

990S-0139452P

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990S-0139453P

990S-0140833P

990S-0140833P

990S-0140833P

990S-014287P

990S-014287P

990S-014287P

990S-014287P

990S-01438BP

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990S-014433BP

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990S-014433BP
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30-APR-1999;
04-MAY-1999;
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16-JUN-1999;
16-JUN-1999;
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        23-APR-1999;
23-APR-1999;
                                                                             07-MAY-1999
                                                                                                    14-MAY-1999
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                                                                                                                                                                                                                      -NDD-80
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                                                                                                                                                                                                                                         100.0%; Score 76; DB 3; Length 82; llarity 100.0%; Pred. No. 5e-06; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                          Zea mays protein fragment SEQ ID NO: 20514.
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990S-0158232P.
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990S-0159331P.
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990S-016964P.
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990S-0160981P.
990S-0160981P.
990S-0160981P.
990S-0161940F.
990S-0161359P.
990S-0161359P.
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990S-0123180P.
990S-0125784P.
990S-0126264P.
990S-0126785P.
990S-0128234P.
990S-0128234P.
990S-0128714P.
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99US-0161993P.
99US-0162142P.
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                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                        Zea mays subsp. mays.
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06-APR-1999;
16-APR-1999;
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990S-0144632P.
990S-0144632P.
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990S-0145086P.
990S-0145088P.
990S-0145088P.
990S-014508P.
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31-AUG-1999;
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06-0CT-1999;
07-0CT-1999;
12-0CT-1999;
13-0CT-1999;
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14-OCT-1999;
14-OCT-1999;
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20-AUG-1999
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence; corn.
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                                                                                                                                                                                                                                                                                                    88;
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ches 0;
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                                                                                                                                                                                                                                                                                                                             Mismatches
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ID AAG18935 standard; protein; 91 AA.
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0
         990S-0159637P-
990S-0159638P-
990S-0160741P-
990S-0160767P-
990S-016070P-
990S-0160814P-
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990S-016136P-
990S-016136P-
990S-016136P-
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990S-016136P-
990S-016136P-
990S-016136P-
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99US-0159331P
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                                                                                                                                                                                                                                                                                                                 Similarity
         14-0CT-1999
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21-0CT-1999
21-0CT-1999
21-0CT-1999
22-0CT-1999
22-0CT-1999
25-0CT-1999
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Local S...
15;
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25-MAR-1999;
29-MAR-1999;
01-APR-1999;
06-APR-1999;
16-APR-1999;
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21-APR-1999;
23-APR-1999;
23-APR-1999;
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30-APR-1999;
30-APR-1999;
04-MAY-1999;
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09-MAR-1999
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Best Local S:
Matches 15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAG18935;
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PR 05-WAY-1999, 990G-0122465P.
PR 06-WAY-1999, 990G-0122465P.
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PR 12-WAY-1999, 990G-012421P.
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PR 10-WAY-1999, 990G-012622P.
P
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01 - JUN - 1999;
04 - JUN - 1999;
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10-JUN-1999;
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18-JUN-1999;
18-JUN-1999;
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16-JUN-1999;
17-JUN-1999;
18-JUN-1999;
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                                                                                                                                                                          Gaps
                                                                                                                                                                          ö
                                                                                                                                                        Length 91;
                                                                                                                                                                         0; Indels
                                                                                                                                                       Score 76; DB 3; I
Pred. No. 5.6e-06;
                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                               Zea mays protein fragment SEQ ID NO: 20832.
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100.0%; Pre
                                                                                                                                                                                                                                                         AAG19142 standard; protein; 95 AA
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990S-0126234P.
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990S-0132486P.
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                                                                                                                                                                         15; Conservative
                                                                                                                                                      Query Match
Best Local Similarity
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30-APR-1999,
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30-APR-1999,
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Matches
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AAG19142
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PR 27-7UL-1999; 99US-0145913P.
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PR 27-CT-1999; 99US-
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                                                                                                     Gaps
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0
                                                                                     Length 95;
                                                                                   Query Match
100.0%; Score 76; DB 3; I
Best Local Similarity 100.0%; Pred. No. 5.9e-06;
Matches 15; Conservative 0; Mismatches 0;
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                                                                                                                      17-OCT-2000 (first entry)
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28-OCT-1999;
29-OCT-1999;
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06-AUG-1999;
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                  10-JUN-1999;
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                                                                                         Gaps
                                                                                         ;
                                                       Length 96;
                                                   100.0%; Score 76; DB 3; Length 96
100.0%; Pred. No. 5.9e-06;
ive 0; Mismatches 0; Indels
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Best Local Similarity 100...
Local Similarity 100...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zea mays subsp. mays.
28-OCT-1999;
29-OCT-1999;
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29-MAR-1999;
01-APR-1999;
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence; corn.
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09-MAR-1999;
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26-0CT-1999;
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Gaps ; 0

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10 - AUG - 1999;
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RESULT 15 ABP42469

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Gaps

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Indels

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ABP42469 standard; protein; 105 AA

(first entry) 22-AUG-2002 ABP42469; 

Human ovarian antigen HOCQG94, SEQ ID NO:3601.

ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndrome; pcOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; infection; cardiovascular disorder; respiratory disorder; neurological disorder; gentrointestinal disorder; urinary system disorder; drug screening; gene therapy; chromosome mapping; forensic analysis; antibody preparation; cytostatic; immunomodulatory; neuroprotective; antiinflammatory; gynaecological; reproductive. Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;

Homo sapiens.

WO200200677-A1

03-JAN-2002.

07-JUN-2001; 2001WO-US018569.

07-JUN-2000; 2000US-0209467P.

(HUMA-) HUMAN GENOME SCI INC.

Birse CE, Rosen CA;

WPI; 2002-147878/19. N-PSDB; ABQ55546.

useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and neurological Isolated nucleic acid molecules encoding novel ovarian polypeptides, diseases.

Claim 11; SEQ ID NO 3601; 2922pp; English.

The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also encompasses polypeptides 90% identical and polymucleotides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host calls comprising human ovarian antigens to polymucleotides against human ovarian antigens and the use of ovarian antigens on preventing various ovary and/or breast related treating, prognosing or preventing various ovary and/or breast cancer, and metastatic tunnurs of ovarian or breast origin, reproductive system disorders (e.g., infertinity, disorders origin, reproductive system disorders (e.g., infertinity, disorders origin, reproductive system disorders (e.g., inflammatory conditions (e.g., mastitis, oophoritis and consistence), immune disorders (e.g., congenital and acquired shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and various ovarian disorders (e.g., anaemia), cardiovascular disorders, inconders (e.g., anaemia), cardiovascular disorders and urinary system disorders. Ovarian antigen polypeptides and polymucleotides may also be used in screening for compounds which modulate ovarian antigen expression or activity. The polymucleotides may further be used for gene therapy, chromosome mapping, in the modulate ovarian antigen expression or activity. The polymucleotides may else used an inference or polypeptides may be used as food additives or to prepare antibodies useful in disease disposis, drug targeting and phenotyping. The present useful in disease diagnosis, drug targeting and phenotyping. The present sequence represents a human ovarian antigen of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO ftp.wipo.int/pub/published_pct_sequences

Length 105; Indels Score 76; DB 5; I Pred. No. 6.5e-06; Mismatches ; 100.0%; 100.0%; Conservative Query Match Best Local Similarity Sequence 105 AA; S

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Search completed: April 8, 2005, 10:50:48
Job time : 63.4 secs

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- protein search, using sw model OM protein April 8, 2005, 09:58:56; Search time 62.4 Seconds (without alignments) 92.971 Million cell updates/sec Run on:

1 LASLSTFQQMWISKQ 15 US-09-423-351C-8 75 Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 segs, 386760381 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2000s:* geneseqp2001s:* geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* A_Geneseq_16Dec04:* geneseqp1980s:* geneseqp1990s:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	Aaw92534 Beta-acti	Adp81223 Protein o	Abg08617 Novel hum	Abp42928 Human ova	Aam81819 Human hae	Aau32061 Novel hum	Abp43127 Human ova	Aam80875 Human hae	Aam81886 Human hae	Aam81332 Human hae	Abo84771 Human can	Abg11441 Novel hum	Ada55146 Human pro	Novel		Abg15466 Novel hum	Abg11440 Novel hum	Adi63068 Human apo	Human	Abp98860 Human str	Aab12985 Human bet	Aap61532 Sequence		Act	Aar49248 Actin. 3/
	ID	AAW92534	ADP81223	ABG08617	ABP42928	AAM81819	AAU32061	ABP43127	AAM80875	AAM81886	AAM81332	AB084771	ABG11441	ADA55146	ABG08618	ABU70549	ABG15466	ABG11440	ADI63068	AD163011	ABP98860	AAB12985	AAP61532	AAR22026	AAR22096	AAR49248
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	Add.62962 Human apo Add.62970 Human apo Add.13002 Human apo Add.13002 Human ste Add.78489 Actin pro Add.14103 Human sar Add.4606 Antipsori
AAR50328 AAW7100 AAW7100 AAW19176 AAB15017 AAY94569 AAB15016 ABB7395 ABB7395 ABB64271 ABM6430 ABM6430 ADB651174 ADF60525	AD163062 AD162970 AD163040 ADL13002 ADL78489 ADL14103 ADN04506
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## ALIGNMENTS

RESULT 1

Peptide substrate; CCT; eukaryotic type II chaperonin complex; cyclin; binding agent; substrate-binding site; SBS; substrate folding; actin; tubulin; treatment; cancer; anticancer drug; viral infection; screening; reduced toxicity. Beta-actin reference peptide substrate #8. AAW92534 standard; peptide; 15 AA (first entry) 26-APR-1999 AAW92534; AAW92534 

WO9853322-A1 26-NOV-1998. Synthetic.

98WO-GB001485. 97GB-00010762 22-MAY-1998; 23-MAY-1997; (CANC-) INST CANCER RES ROYAL CANCER HOSPITAL.

Liou AK; Hynes G, Willison K,

WPI; 1999-070162/06.

Identifying specific binding agents for substrate binding site in CCT chaperonin complex - also new peptide binding agents and their mimetics, and peptides containing a specific CCT binding site, used for treating cancer.

Disclosure; Fig 10; 97pp; English.

This invention describes a method which uses the CCT (eukaryotic type II chaperonin) complex or part of it, for identifying a binding agent that can occupy a substrate-binding site (SBS) on the CCT complex. By binding to the CCT complex, the binding agents block an SBS so that biological activity of the CCT complex is affected, particularly its ability to fold substrates such as actin, tubulin and cyclin. The binding agents are useful for treatment of cancer, particularly when used in combination with an anticancer drug, or viral infections. Nucleic acid fragments are used to screen for agents, e.g. binding agents that modulate interaction between the CCT complex and a protein that is to be folded. The binding

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RESULT
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                 (unlike known microtubule-stabilising agents that affect all cells), so should have reduced toxicity for normal cells. AAM92527-W92541 are peptide substrates used in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New ovarian specific nucleic acid molecules and polypeptides useful for diagnosing, preventing or treating ovarian cancer, for producing transgenic animals or cells, or for research purposes.
                                                                                                                                                                                                             Gaps
    agents may target cells that are actively synthesising tubulin etc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ovarian; ovarian specific nucleic acid; OSNA; vaccine; cytostatic; human.
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                                                                                                                                                              Score 75; DB 2; Length 15; Pred. No. 6.5e-06; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein of human ovarian specific gene, SEQ ID No 257.
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                                                                                                                                                                                                                                                                                                                                                                                                                          ADP81223 standard; protein; 48 AA.
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2002US-0431321P.
2003US-0484584P.
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Best Local Similarity 100.
Matches 15, Conservative
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N-PSDB; ADP81063.
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metastatic; cancer;
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                                                                                                                       Sequence 15 AA;
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30-JUN-2003;
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ADP8 1223
ADP8 1223
ADP 1223
ADP 1223
ADP 109-5
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The invention relates to isolated polynucleotide (I) and polypeptide (II)

sequences. (I) is useful as hybridisation probes, polymerase chain

caction (PCR) primers, oligomers, and for thromesome and gene mapping,

and in recombinant production of (II). The polynucleotides are also used

in diagnostics as expressed sequence tags for identifying expressed

genes. (I) is useful in gene therapy techniques to restore normal

activity of (II) or to treat disease states involving (II). (II) is

useful for generating antibodies against it, detecting or quantitating a

cusclul for generating antibodies against it, detecting or quantitating a

polypeptide in tissue, as molecular weight markers and as a food

supplement. (II) and its binding partners are useful in medical imaging

of sites expressing (II). (I) and (II) are useful for treating disorders

involving aberrant protein expression or biological activity. The

polypeptide and polynucleotide sequences have applications in

diagnostics, forensics, gene mapping, identification of mutations

responsible for genetic disorders or other traits to assess biodiversity
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polypeptide; a method of treating a patient with ovarian cancer; and a vaccine comprising the above polypeptide or nucleic acid encoding the polypeptide. The isolated nucleic acid molecules and polypeptides have cytostatic activity. The isolated polypeptides may be used to create a vaccine. The isolated nucleic acid molecules and polypeptides can be used co diagnosing or monitoring the presence and metastases of ovarian cancer and treating ovarian cancer. This sequence represents the protein of an ovarian specific gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                Score 75; DB 8; Length 48; Pred. No. 2.2e-05;
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100.0%;
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2000US-00649167.
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N-PSDB; AAS72804.
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Best Local Similarity
Matches 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                              Sequence 48 AA;
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23-AUG-2000;
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RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP41228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also encompasses polypeptides 90% identical and polymucleotides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigen polymucleotides, antibodies against human ovarian antigens, and the use of ovarian antigen polymucleotides and polypeptides in diagnosing, treating, prognosing or preventing various ovary and/or breast-related disorders. Such conditions include ovarian cancer and breast cancer, and metastatic tumours of ovarian or breast origin, reproductive system
and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                    ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndrome; PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; infection; cardiovascular disorder; respiratory disorder; neurological disorder; gestrointestinal disorder; urinary system disorder; drug screening; gene therapy; chromosome mapping; forensic analysis; antibody preparation; cytostatic; immunomodulatory; neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ov. cancer), immune disorders, cardiovascular disorders and neurological
                                                                                                                                                Gaps
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                                                                                                                 Score 75; DB 4; Length 86; Pred. No. 4e-05;
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                                                                                                                              red. No. 4e-05;
Mismatches (
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0
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                                                                                                                                                                                          LASLSTFQQMWISKQ 71
                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                Conservative
                                                                                                                                                                        1 LASLSTFQQMWISKQ
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                                                                                                                   Query Match
Best Local Similarity
Matches 15; Conserv
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                                                                                          Sequence 86 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
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disorders (e.g., infertility, disorders of pregnancy, anovulation, colycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine disorders, infertions (e.g., chlamydia, HV, toxoplasmosis, and toxic shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and cypic immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus), communodeficiencies, autoimmune oophoritis, systemic lupus erythematosus), chlood-related disorders (e.g., anamia), cardiovascular disorders.

CC respiratory disorders, neurological disorders, gastrointestinal disorders and urinary system disorders. Ovarian antigen polypeptides and compute ovarian antigen be used in screening for compounds which modulate ovarian antigen be used in screening for compounds which continues be used for gene therapy, chromosome mapping, in the citerther be used for gene therapy, chromosome mapping, in the collection of individuals and in forensic analysis, and the collection of individuals and in forensic analysis, and the collection of individuals and in forensic analysis. The present sequence represents a human ovarian antigen of the invention. Note: The sequence data for this patent did not form part of the printed sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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100.0%; Pred. No. 5.2e-05;
ive 0; Mismatches 0;
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2000US-0218950P.
2000US-0222903P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-514842/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 110 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200164886-A2.
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Local Sim.
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                                                                                                                          present sequence is the protein sequence of a human haematological malignancy related antigen. The methods of the present invention comprise detecting the presence of haematological malignancy related antigen (s) in a sample obtained from the patient (an increased level of the polypeptide, compared to an unaffected individual, is indicative of an increased risk). Haematological malignancies which can be treated using the present invention are chronic lymphocytic leukaemia, lymphoma, follicular lymphoma, hodgkin's lymphoma, non-Hodgkin's lymphoma and T/B cell non-Hodgkin's lymphoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids encoding a range of human polypeptides, useful in genetic
                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       stem cell proliferation; haematopoiesis; nerve tissue regeneration;
immune suppression; immune stimulation; anti-inflammatory; leukaemia.
                                                                                       The present invention relates to compositions and methods for the detection, diagnosis and therapy of haematological malignancies. The
e.g. chronic lymphocytic leukemia, lymphoma, follicular lymphoma and
Hodgkin's and T/B cell non-Hodgkin's lymphoma.
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                                                                                                                                                                                                                                                                                                                                                   Length 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; vaccination; gene therapy; nutritional supplement;
                                                                                                                                                                                                                                                                                                                                                  Score 75; DB 4; Length 12
Pred. No. 6.2e-05;
Mismatches 0; Indels
                                                   Claim 1; Page 1114; 1252pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU32061 standard; protein; 135 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel human secreted protein #2552,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vaccination, testing and therapy.
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100.0%;
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26-JAN-2001; 2001US-00770160
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Best Local Similarity 100.
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tang YT, Liu C,
                                                                                                                                                                                                                                                                                                                 Sequence 129 AA;
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                                                                         and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid sequences of novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndrome; PCOS; ovarian cyst; dysmenorrhoes; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; infection; cardiovascular disorder; respiratory disorder; neurological disorder; genstrointestinal disorder; urinary system disorder; drug screening; gene therapy; chromosome mapping; forensic analysis; antibody preparation; cytosteatic; immunomodulatory; neuroprotective; antiinflammatory; gynaecological; reproductive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP41228) and to cDMAs encoding them (ABD44131-ABD56305), and also encompasses polypeptides 90% identical and polynucleotides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigen polynucleotides, antibodies against human ovarian antigens, and the use of ovarian antigen polynucleotides and polypeptides in diagnosing, treating, prognosing or preventing various ovary and/or breast-related
to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopoiesis; and in bone, cartilage, tendor
                                                                                                                                                                                                                                                       Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               useful in the prevention, treatment and diagnosis of cancer (e.g. ov. cancer), immune disorders, cardiovascular disorders and neurological diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated nucleic acid molecules encoding novel ovarian polypeptides,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ovarian antigen; ovary; ovarian; breast; cancer; tumour;
                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                 Length 135;
                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                               100.0%; Score 75; DB 4; I
100.0%; Pred. No. 6.5e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human ovarian antigen HVVBD91, SEQ ID NO:4259.
                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 11; SEQ ID NO 4259; 2922pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                             ABP43127 standard; protein; 145 AA.
                                                                                                                                       secreted proteins of the invention
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                                                                                                                                                                                                                                                                                                                               LASLSTFOOMWISKO 111
                                                                                                                                                                                                                                                                                           15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                           1 LASLSTFOOMWISKO
                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                             Sequence 135 AA;
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                                                                                                                                                                                                                   Local S. 15;
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                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                     Matches
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disorders .ucc conditions include Ovarian cancer and Dreast Cancer, and metastatic tumours of ovarian or breast origin, reproductive system disorders (e.g., infertility, disorders of pregnancy, anovulation, colorycatic ovary syndrome, ovarian cysts, and dymemorrhoes), endocrine disorders infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and vaginitis), immune disorders (e.g., congenital and acquired immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus), blood-related disorders (e.g., anaemia), cardiovascular disorders and unimary system disorders. Ovarian antigen polypeptides and polymucleotides may also be used in screening for compounds which collustication of individuals and in forensic analysis, and the identification of individuals and in forensic analysis, and the sequence represents a human ovarian antigen of the invention. Note: The sequence data for this patent did not form part of the printed sequence data for this patent did not form part of the printed sequence data for this patent did not form part of the printed sequence in the printed sequence fare for this patent did not form part of the printed sequence in the patent did not form part of the printed sequence in the patent did not form part of the printed sequence in the patent did not form part of the printed sequence in the patent did not form part of the printed sequence in the patent did not form part of the printed sequence in the patent did not form part of the printed sequence in the patent did not form part of the printed sequence in the patent did not form part of the printed sequence in the patent did not form part of the printed sequence in the patent did not form part of the printed sequence in the patent did not form part of the printed sequence in the patent did not form part of the printed sequence in the patent did not form part of the printed sequence in the patent did not form part of the printed sequence in the patent did not form 
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haematological malignancy, antigen, chronic lymphocytic leukaemia,
follicular lymphoma, Hodgkin's lymphoma, non-Hodgkin's lymphoma.
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Pred. No. 7e-05;
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disorders. Such conditions include
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28-APR-2000; 2000US-020099P.
01-MAY-2000; 2000US-0200999P.
22-MAY-2000; 2000US-0202084P.
14-JUL-2000; 2000US-0218950P.
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nes 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seguence 145 AA;
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17-MAR-2000;
27-APR-2000;
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                                                                                                    The present invention relates to compositions and methods for the detection, diagnosis and therapy of haematological malignancies. The present sequence is the protein sequence of a human haematological malignancy related antigen. The methods of the present invention comprise detecting the presence of haematological malignancy related antigen(s) in a sample obtained from the patient (an increased level of the polypeptide, compared to an unaffected individual, is indicative of an increased risk). Haematological malignancies which can be treated using the present invention are chronic lymphocytic leukaemia, lymphoma, follicular lymphoma, non-Hodgkin's lymphoma and T/B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Compositions and methods for the detection of hematological malignancies, e.g. chronic lymphocytic leukemia, lymphoma, follicular lymphoma and
           Compositions and methods for the detection of hematological malignancies, e.g. chronic lymphocytic leukemia, lymphoma, follicular lymphoma and Hodgkin's and T/B cell non-Hodgkin's lymphoma.
                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; cytostatic; vascular; gene therapy; vaccine; lymphoma;
haematological malignancy; antigen; chronic lymphocytic leukaemia;
follicular lymphoma; Hodgkin's lymphoma; non-Hodgkin's lymphoma.
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                                                                                                                                                                                                                                                                                                                                     100.0%; Score 75; DB 4; Length 147; 100.0%; Pred. No. 7.1e-05;
                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human haematological malignancy-related antigen #1584.
                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                           Claim 1; Page 743-744; 1252pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAM81886 standard; protein; 147 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mannion J;
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2000US-0190479P.
2000US-0200545P.
2000US-0200303P.
2000US-02003779P.
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2000US-0202084P.
2000US-0206201P.
2000US-0218950P.
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04-AUG-2000; 2000US-0223416P.
07-AUG-2000; 2000US-0223378P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2001; 2001WO-US007272
                                                                                                                                                                                                                                                                                                                                                                                                                                     118 LASLSTFOOMWISKO 132
                                                                                                                                                                                                                                                                                                                                                                                                       1 LASLSTFOOMWISKO 15
                                                                                                                                                                                                                                                                          cell non-Hodgkin's lymphoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                   Query Match 100.
Best Local Similarity 100.
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                       Sequence 147 AA;
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14-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAM81886;
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AAM81886
XTTTXXXXCCCCCCCCXXX
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                                                      The present invention relates to compositions and methods for the detection, diagnosis and therapy of haematological malignancies. The present sequence is the protein sequence of a human haematological malignancy related antigen. The methods of the present invention comprise detecting the presence of haematological malignancy related antigen (8) in sample obtained from the patient (an increased level of the polypeptide, compared to an unaffected individual, is indicative of an increased risk). Haematological malignancies which can be treated using the present invention are chronic lymphocytic leukaemia, lymphoma, follicular lymphoma, Hodgkin's lymphoma, non-Hodgkin's lymphoma and T/B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Compositions and methods for the detection of hematological malignancies, e.g. chronic lymphocytic leukemia, lymphoma, follicular lymphoma and Hodgkin's and T/B cell non-Hodgkin's lymphoma.
                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human, cytostatic, vascular, gene therapy, vaccine, lymphoma,
haematological malignancy, antigen, chronic lymphocytic leukaemia,
follicular lymphoma, Hodgkin's lymphoma, non-Hodgkin's lymphoma.
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                                                                                                                                                                                                                                                                          Length 147;
                                                                                                                                                                                                                                                         Score 75; DB 4; Lengtn La Pred. No. 7.1e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human haematological malignancy-related antigen #1030.
Hodgkin's and T/B cell non-Hodgkin's lymphoma
                            Claim 1; Page 1141; 1252pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                    AAM81332 standard; protein; 147 AA
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28-APR-2000; 2000US-0200979-
01-MAY-2000; 2000US-0200999-
04-MAY-2000; 2000US-020084P-
22-MAY-2000; 2000US-0206201P-
14-UUL-2000; 2000US-0218950P-
03-AUG-2000; 2000US-0218950P-
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                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                   Local Similarity
nes 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-514842/56.
                                                                                                                                                                                                                                         Sequence 147 AA;
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27-APR-2000;
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Matches
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Claim 1; Page 925; 1252pp; English.

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The present invention relates to compositions and methods for the detection, diagnosis and therapy of haematological malignancies. The present sequence is the protein sequence of a human haematological malignancy related antigen. The methods of the present invention comprise detecting the presence of haematological malignancy related antigen (8) in sample obtained from the patient (an increased level of the polypeptide, compared to an unaffected individual, is indicative of an increased risk). Haematological malignancies which can be treated using follicular lymphoma, Hodgkin's lymphoma, non-Hodgkin's lymphoma and T/B cell non-Hodgkin's lymphoma and T/B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             associated (CA) nucleic acids encoding them. The invention also relates to a method for treating cancers involving administering to a patient an inhibitor of CAP, and a method of screening for anticancer activity in a potential drug involving providing a cell that expresses a CA gene, contacting a tissue sample derived from a cancer cell with an anticancer drug candidate and monitoring the effect of the anticancer drug candidate on expression of the CA gene. The CAP proteins are useful for detecting and for screening for a bioactive agent capable of modulating the activity of a CAP protein in a test cell sample and for screening for a bioactive agent capable of modulating the activity of a CAP protein. The CA nucleic acids are useful for diagnosing cancer, involving determining the expression of a CA nucleic acid in a tissue. This sequence represents a human CAP of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel human cancer associated protein encoded within open reading frame of cancer associated gene, useful as targets for diagnosing cancer.
                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to cancer-associated proteins (CAP) and the
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                                                                                                                                                                                                                                                                                                      100.0%; Score 75; DB 4; Length 147; 100.0%; Pred. No. 7.1e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cancer-associated protein; CAP; cancer; cytostatic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABO84771 standard; protein; 149 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-DEC-2002; 2002US-00322281.
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                                                                                                                                                                                                                                                                                                                                                                                       15
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                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                     1 LASLSTFOOMWISKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Morris DW, Malandro MS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2004-499109/47.
                                                                                                                                                                                                                                                                                                                       Local Similarity
les 15; Conserv
                                                                                                                                                                                                                                                                Sequence 147 AA;
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                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                            Matches
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Query Match
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Local 15; Conserve
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Sequence 181 AA;
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                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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                                                                                                                                                                                                 ADA55146;
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                                                                                                                                               RESULT 13
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ID ABG0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain recardion (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal crivity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving abberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess blodiversity represent cold sequences. Aggonolo-Abg30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this pattent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at (ftp. wipo.int/pub/published_pot_esservers)
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                                                                              Gaps
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                                                                                                                                                                                                                                                                                                           Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder.
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                                                    Length 149;
                                                                            0; Indels
                                                   100.0%; Score 75; DB 8; I
100.0%; Pred. No. 7.2e-05;
at ftp.wipo.int/pub/published_pct_sequences
                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 20; SEQ ID NO 41800; 103pp; English.
                                                                                                                                                                                                                                                                                 Novel human diagnostic protein #11432
                                                                                                                                                                                                 ABG11441 standard; protein; 181 AA
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23-AUG-2000; 2000US-00649167.
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                                                                                                                       120 LASLSTFQQMWISKQ 134
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                                                                                                       1 LASLSTFOOMWISKO 15
                                                                                                                                                                                                                                                      (first entry)
                                               Query Match
Best Local Similarity 100.
Matches 15; Conservative
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N-PSDB; AAS75628.
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                         Sequence 149 AA;
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Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diseases in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polynucleotides encoding full-length polypeptides, e.g. secretory and/or membrane proteins, useful for developing medicines for disease which the gene is involved, or as target molecules for gene therapy.
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Score 75; DB 4; Length 18 Pred. No. 8.8e-05; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                    ADA55146 standard; protein; 197 AA.
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(REAS-) RES ASSOC BIOTECHNOLOGY.
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0
   100.0%;
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24-JAN-2002; 2002US-0350435P.
                                                                                                                                                                               152 LASLSTFOOMWISKO 166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 LASLSTFQQMWISKQ 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human protein, SEQ ID 2714.
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nes 15; Conservative
                                                               Conservative
                                                                                                                         1 LASLSTFOOMWISKO
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Human, prey, adipocyte, SID, selected interacting domain; anorectic; antidiabetic, protein-protein interaction; diabetes; yeast 2-hybrid assay; metabolic disorder; obesity.

14-MAR-2002; 2002WO-EP003768 14-MAR-2001; 2001US-0275734P

WO200286122-A2. Homo sapiens

31-OCT-2002

Daviet L;

Legrain P,

WPI; 2003-103412/09. N-PSDB; ACA57093.

(HYBR-) HYBRIGENICS.

Human adipocyte Selected Interacting domain, SID, #180.

10-JUN-2003 (first entry)

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PGR) primers, oligomers, and for chomosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving abbarrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic patent did not appear in the printed specification, but was obtained in the vival out. Every man obtained in the printed specification, but was obtained in the vival.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
                                                                                                                                                                                                                                            Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                                                               Novel human diagnostic protein #8609.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-MAR-2000; 2000US-00540217, 23-AUG-2000; 2000US-00649167,
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                                                                                 (first entry)
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Matches 15; Conserve
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                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                 13-FEB-2002
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ABG08618
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New complex between two interacting proteins in adipocyte cells, useful for identifying selected interacting domains that modulate protein interactions, or for preventing or treating metabolic disorders such as

Claim 6; Page 167; 382pp; English.

obesity or diabetes

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The invention relates to a complex between two interacting proteins in adipocyte cells, given in the specification. The proteins are identified by selected a bait protein from a known adipocyte marker and then performing a yeast 2-hybrid selection to isolate prey proteins encoded by correct companies of an adipocyte cDNA library. The proteins are designated SID (RTW) (selected interacting domains) proteins. Also included are a polymetheotide encoding a polypeptide in the adipocyte cells, a compinent host cell expressing at least one of the interacting cells, a recombinant host cell expressing at least one of the interacting cells, a sID (RTW) polypeptide comprising any of the 738 amino acid sequences given in the specification (including its fragment or variant), a vector cells, a SID (RTW) polymelectide, and its fragment or variant), a vector comprising the SID (RTW) polymuclectide, a recombinant host cell comprising the vector, a protein chip comprising the polypeptides and a recombinant host cell comprising all or part of the data, listed in the specification. The complex, polymelectides are useful for preventing or treating metabolic disorders such as obesity or diabetes. The polymuclectides are useful for preventing or treating metabolic disorders such as obesity or diabetes. CT the polymuclectides are useful for identifying selected interaction thus particularly useful for identifying selected interaction thus certains the therapeutic effect. The present sequence represents a SID (Arrw), protein of the data sequence represents a SID (Arrw) and the second of the sequence represents a SID (Arrw) and the sequence of the sequence represents a SID (Arrw) and the sequence of the sequence represents a SID (Arrw) and the sequence of the sequence represents a SID (Arrw) and the sequence of the sequence of the sequence represents a SID (Arrw) and the sequence of the sequenc
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8, 2005, 10:50:47

Search completed: April Job time : 63.4 secs

ABU70549 standard; protein; 274 AA.

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Sequence 6, Application US/08609236
| Sequence 6, Application US/08609236
| Patent No. 6087398
| CENERAL INFORMATION:
| TITLE OF INVENTION: No. 6087398el Sickle Cell Anemia Treatment
| TITLE OF INVENTION: No. 6087398el Sickle Cell Anemia Treatment
| NUMBER OF SEQUENCES:
| ADDRESSEE: Addler, LLP | STREET: 8011 Candle Lane | STREET: 18011 Candle Lane | CITY: Houston | STATE: Texas | CONTRY: USA | COMPUTER READABLE FORM:
                      US-09-949-016-10409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , ORGANISM: Human
US-09-949-016-10409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7, Apple Sequence 731, Apple 2, Appli
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Sequence 8, Appli
Sequence 8, Appli
Sequence 610, Appl
Sequence 10757, A
Sequence 2, Appli
Sequence 2, Appli
Sequence 33348, A
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9424, Ap
11313, A
4, Appli
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Sequence 6, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                                  April 8, 2005, 09:58:57; Search time 17.5333 Seconds (without alignments) 63.863 Million cell updates/sec
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                      GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-106-217-3

US-09-919-172-33

US-09-919-172-33

US-09-919-172-33

US-09-919-112-33

US-09-949-016-1721

US-09-949-016-17313

US-09-949-016-11313

US-09-17-137A-8

US-09-17-137A-8

US-09-17-137A-8

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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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Sequence 10409, Application US/09949016

Batent No. 6812339

GENERAL INFORMATION:
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION NUMBER: US/09/949,016
CURRENT APPLICATION NUMBER: 60/241,755
FILMS REPELICATION NUMBER: 60/241,755
PRIOR PILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-00-03
PRIOR PILING DATE: 2000-00-03
PRIOR PILING DATE: 2000-00-03
NUMBER OF SEQ ID NOS: 207012
SEQ ID NOS: 207012
SEQ ID NO 10409
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                                                                                 Sequence 395, App
Sequence 744, App
Sequence 746, App
Sequence 8246, App
Sequence 626, App
Sequence 55366, A
                                                                                                                                                                                                                                    Sequence 13505, A
Sequence 6616, Ap
Sequence 4655, Ap
Sequence 26038, A
Sequence 6024, Ap
Sequence 8, Appli
Sequence 8, Appli
6656, Ap
8452, Ap
14108, A
18965, A
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13505, A
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                  US-09-949-016-8452
US-09-248-796A-14108
US-09-248-796A-18965
US-09-538-092-395
US-09-198-452A-794
US-09-349-016-8246
US-09-349-016-8246
US-09-270-767-40150
US-09-270-767-55366
US-09-328-352-6451
US-09-328-352-6616
US-09-328-352-4655
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US-09-328-352-4655
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US-09-328-352-4655
US-09-328-352-4655
US-09-361-681A-6024
US-09-318-352-4655
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US-09-318-352-4655
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                210 LASLSTFOOMWISKO 224
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Best Local Similarity 100.
Matches 15; Conservative
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AND -ACTIN AND THEIR USE IN FILAMENTOUS FUNGI EXPRESSION, SECRETION AND ANTISENSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 3-1/4" Disk 1.44MB
COMPUTER: IBM PC compatible
SOFTWARE: WOOTGPEFFECT 8 for Windows
CURRENT APPLICATION DATA:
RPLICATION NUMBER: US/09/171,337A
FILING DATE: 14-May-1999
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     U-011948-3
                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 75; DB 3; Length 375; 100.0%; Pred. No. 4.3e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: BARREDO FUENTE, JOSE LUIS
RODRIGHEZ SAIZ, Marta
COLLADOS DE LA VIEJA, Alfonso J.
MORENO VALLE, Migeul Angel
SALTO MALDONADO, Francisco
DIEZ GARCIA, Bruno
TITLE OF INVENTION: PROMOTERS OF THE GENES GLUTAMATE
DESHYDROGENASE, -N-ACETYLHEXOSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (C) REF./DOCKET NO.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/ES98/00056
FILING DATE: 5-MAR.1998
APPLICATION NUMBER: ES9700482
FILING DATE: 5-MAR.1997
ATTORNEY/AGENT INFORMATION:
NAME: MASS, Clifford J.
                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                             2323-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 30,086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: LADAS & PARRY
STREET: 26 WEST 61 STREET
CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              // Sequence 7, Application US/09171337A
// Patent No. 6300095
// GENERAL INFORMATION:
                                  CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Saxe, Stephen A.
REGISTRATION NUMBER: 38,609
REFERENCE/DOCKET NUMBER: 2323-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-783-6040
TELEFAX: 202-783-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 233288
INFORMATION FOR SEQ 1D NO: 7
SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acids
TYPE: amino acids
                                                                                                                                                                             TELEFAX: 202-783-6031
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                346 LASLSTFOOMWISKO 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 LASLSTFOOMWISKO 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0
Matches 15; Conservative
                                                                                                                                                                                                                                                                                 ; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-106-217-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: NY
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Patent No. 6063576
GENERAL INFORMATION:
APPLICANT: Clson, Timothy M.
TITLE OF INVENTION: Actin Mutations in Dilated
TITLE OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
STREET: 555 Thirteenth Street, N.W., Suite 701 East
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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Pred. No. 4.3e-05;
Mismatches 0; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/106,217
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word for Macintosh
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/609,236
FILING DATE: March 1, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/002,288
FILING DATE: August 14, 1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Benjamin Aaron Adler, Ph.D.
REGISTRATION NUMBER: 35,423
REBRENCE/DOCKET NUMBER: D5807
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-777-2321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0%; Partches 15; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 345 LASLSTFQQMWISKQ 359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: Linear MOLECULE TYPE: DESCRIPTION: Protein HYPOTHETICAL: No FRAGMENT TYPE: ORIGINAL SOURCE: STRAIN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: Amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                U.S.A.
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APPLICANT: Furness, Michael
APPLICANT: Furness, Michael
APPLICANT: Furness, Michael
APPLICANT: Buchbinder, Jenny
TITLE OP INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
FILE REPERENCE: PA-0041 US
CURRENT APPLICATION NUMBER: US/09/976,594
CURRENT FILING DATE: 2000-10-12
PRIOR APPLICATION NUMBER: 60/240,409
PRIOR FILING DATE: 2000-10-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:

APPLICANT: Keating, Mark T.

APPLICANT: Olson, Timothy M.

TITLE OF INVENTION: Actin Mutations in Dilated

TITLE OF INVENTION: Cardiomyopathy, a Heritable Form of Heart Failure
NUMBER OF INVENTION: 18

CORRESPONDENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.

STREET: 555 Thirteenth Street, N.W., Suite 701 East
STREET: Tower
                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                Query Match
100.0%; Score 75; DB 4; Length 375;
Best Local Similarity 100.0%; Pred. No. 4.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 75; DB 4; Length 375; 100.0%; Pred. No. 4.3e-05;
                                                                 OTHER INFORMATION: amino acid sequence of the protein with a molecular weight of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. 6673549 1837317CD1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                   ORGANISM: Penicillium chrysogenum
                                                                                                                41760 Da.
SEQUENCE DESCRIPTION: SEQ ID NO: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-976-594-731
; Sequence 731, Application US/09976594
; Patent No. 6673549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 2, Application US/09106217; Patent No. 6063576
                                                                                                                                                                                                                                                                                                                                                   346 LASLSTFOOMWISKO 360
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15; Conservative
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SOFTWARE: PERL Program
SEQ ID NO 731
LENGTH: 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Washington
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STATE: DC
COUNTRY:
                                         FEATURE
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US-09-106-217-2
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MEDIUM TYPER: 3-1/4" Disk 1.44MB

COMPUTER: IBM PC compatible
OPERATING SYSTEM: Microsoft Windows for Workgroups 3.11
SOFTWARE: WordPerfect 8 for Windows
SOFTWARE: WordPerfect 8 for Windows
SOFTWARE: WordPerfect 8 for Windows
CURRITY APPLICATION DATA:
APPLICATION NUMBER: US/09/631,022
FILING DATE: 10-May-1999
RIGATION NUMBER: 09/171,337
FILING DATE: 14-May-1999
APPLICATION NUMBER: PCT/ES98/00056
FILING DATE: 5-Mak-1997
ATTORNEY/AGENT INFORMATION:
NAME: MASS, Clifford J.
REGISTRATION NUMBER: 30,086
REGISTRATION NUMBER: 30,086
                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7, Application US/09631022
Patent No. 6558921
GENERAL INPORMATION:
RAPLICANT: BARREDO FUENTE, Jose Luis
APPLICANT: BARREDO FUENTE, Marta
COLLADOS DE LA VIELA, Alfonso J.
MORENO VALLE, Migeul Angel
SALTO MALDONADO, Francisco
DIEZ GARCIA, Bruno
TITLE OF INVENTION: PROMOTERS OF THE GENES GLUTAMATE
DESHYDROGENASE, -N-ACETYLHEXOSAMINIDASE
AND -ACTIN AND THEIR USE IN FILAMENTOUS
FUNGI EXPRESSION, SECRETION AND ANTISENSE
                                                                                                                                   OTHER INFORMATION: amino acid sequence of the -actin protein with a molecular weight of
                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                 Length 375;
                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                              100.0%; Score 75; DB 3; 100.0%; Pred. No. 4.3e-05;
                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                          ORGANISM: Penicillium chrysogenum
                                                                                                                                                                                                          SEQUENCE DESCRIPTION: SEQ ID NO: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 20
CORRESPONDENCE ANDRESS:
ADDRESSEE: LADDAS & PARRY
STREET: 26 WEST 61 STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acids
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                      346 LASLSTFQQMWISKQ 360
                                                                                                                                                                                                                                                                                                                                                                           1 LASLSTFOOMWISKO 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 10023
COMPUTER READABLE FORM:
                        TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.09
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: NY
COUNTRY: USA
                                                                                                                                                                                         41760 Da.
                                                                                                                  FEATURE
                                                                                                                                                                                                                                  US-09-171-337A-7
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TYPE: PRT
ORGANISM: Human
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                                                                                                                                                TYPE: PRT
                                                                                                                                                                                                                                          Query Match
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Sequence 53, Application US/09917254
Setent No. 6703204
Setent No. 6703204
Setent No. 6703204
TGREANT: Mutter, George
APPLICANT: Baak, Jan
TITLE REPERENCE: B0801/7224 (JRV)
FILE REPERENCE: B0801/7224 (JRV)
CURRENT APPLICATION NUMBER: US/09/917,254
CURRENT FILING DATE: 2001-07-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 75; DB 4; Length 377; 100.0%; Pred. No. 4.3e-05; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc feature; OTHER INFORMATION: Incyte ID No. 6673545 1709118CD1
US-09-919-172-33
SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/106,217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 75; DB 3; 1
Pred. No. 4.3e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KESULI 8
Sequence 33, Application US/09919172
Fatent No. 6673545
GENERAL INFORMATION:
APPLICANT: Faris, Mary
TILE OF INVENTION: PROSTATE CANCER MARKERS
FILE REPERENCE: PA-0036 US
CURRENT APPLICATION NUMBER: US/09/919,172
CURRENT APPLICATION NUMBER: 00/222,469
FRIOR APPLICATION NUMBER: 60/222,469
FRIOR APPLICATION NUMBER: 60/222,469
FRIOR PILLING DATE: 2000-07-30
FRIOR APPLICATION NUMBER: 60/222,469
FRIOR FILLING DATE: 2000-07-36
SOFTWARE: PERL PROGRAM
SEQ ID NO 33
LENGTH: 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
100.0%; Score 75; DB
Best Local Similarity 100.0%; Pred. No. 4.3
Matches 15; Conservative 0; Mismatches
                                                                                    CLASSIFICATION:
ATTORNEY AGENT INFORMATION:
NAME: Saxe, Stephen A.
REGISTRATION NUMBER: 38,609
REFERENCE/DOCKET NUMBER: 2323-125
TELEPHONE: 202-783-6040
TELEPHONE: 202-783-6031
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 377 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   348 LASLSTFOOMWISKO 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            348 LASLSTFOOMWISKO 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 LASLSTFOOMWISKQ 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 LASLSTFQQMWISKQ 15
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Best Local Similarity 100.0
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                        , MOLECULE TYPE: protein US-09-106-217-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-917-254-53
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RESULT 10
US-09-248-796A-14109
US-09-248-796A-14109

Sequence 14109, Application US/09248796A

Patent No. 6747137

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN:
TITLE OF INVENTION: PCA DE DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: NO US 00/074,796A

CURRENT APPLICATION NUMBER: US 60/074,725

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR APPLICATION NUMBER: US 60/096,409

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 14109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7721, Application US/09949016

Sequence 7721, Application US/09949016

Batent No. 681239

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

ATILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: 60/241,755

CURRENT FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FASTSEQ for Windows Version 4.0

LENGTH: 386
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100.0%; Pred. No. 4.3e-05;
                                                                                                                                                                                                                                                                     red. No. 4.3e-05;
Mismatches 0;
PRIOR APPLICATION NUMBER: US 60/222,093
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 102
SEG ID NO 53
LENGTH: 377
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348 LASLSTFQQMWISKQ 362
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                                                                                                                                                                                                                                                                                                                                            1 LASLSTFOOMWISKO 15
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Best Local Similarity 100.0
Matches 15; Conservative
                                                                                                                                                                                                                                                                Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Candida albicans
                                                                                                                                                                     ; ORGANISM: Homo Sapiens
US-09-917-254-53
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US-08-494-151-14

Sequence 14, Application US/08494151

Patent No. 5840528

GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TYPLE OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/494,151
FILING DATE: 23-JUN-1995
CLASSIFICATION: 435
ATTONENY/AGENT INPORMATION:
NAME: Mursahige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 29,959
TELEPHONIN CATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEPHONE: (202) 887-0763
                                                                                                                                                                                                                                  Sequence 4, Application US/09700436;
Batent No. 6482802
GENERAL INPORMATION:
APPLICANT: Hu, Guo-Fu
APPLICANT: Vallee, Burt L.
TITLE OF INVENTION: ANGIOGENESIS RELATED DISEASES
FILE REFERENCE: 9457-008-99
CURRENT APPLICATION WHMBER: US/09/700,436
CURRENT FILING DATE: 2000-11-09
PRIOR RPLICATION NUMBER: CCT/US99/10269
PRIOR RILING DATE: 1999-05-11
PRIOR FILING DATE: 1999-05-11
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 70; DB 4; Le
Pred. No. 1.5e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93.3%; Scc. No. 100.0%; Pred. No. . . . . . . . . . . . . . . Mismatches
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                         375 LASLSTFQQMWISKQ 389
                                 1 LASLSTFOOMWISKO 15
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Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo Sapiens
                                                                                                                                                                                                                     US-09-700-436-4
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Sequence 1313, Application US/09949016

Batent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR PILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 2000-09

SEQ ID NOS: 2000-09

SEQ ID NOS: 2000-09

SEQ ID NO 11133

SEQ ID NO 11133
                                                                                                                                                                                                                                                                                                                                                                    US-09-949-016-9424

i Sequence 9424, Application US/09949016

j Patenn No. 6812339

j GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT FILING DATE: 2000-04-14

PRIOR PAPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR PILING DATE: 2000-10-03

SPRIOR PILING DATE: 2000-10-03

SPRIOR FILING DATE: 2000-10-03

SPRIOR FILING DATE: 2000-10-03

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PRIOR PLING DATE: 2000-10-03

PRIOR PLING DATE: 2000-10-03

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SPRIOR PLING DATE: 2000-10-03

PRIOR PRIOR DATE: 2000-10-03

PRIOR PLING DATE: 20
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                                                               Length 386;
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                                                           100.0%; Score 75; DB 4; 100.0%; Pred. No. 4.5e-05;
                                                                                                                           Mismatches
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Matches 15; Conservative
                          Query Match
Best Local Similarity 100...
Best Local 5; Conservative
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Best Local Similarity 100.
Matches 15; Conservative
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-949-016-11313
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; ORGANISM: Human
US-09-949-016-11313
US-09-949-016-7721
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Gaps

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Sequence 1696, Ap Sequence 2250, Ap Sequence 1239, Ap Sequence 1250, Ap Sequence 2250, Ap Sequence 2250, Ap Sequence 2250, Ap Sequence 2250, Ap Sequence 2350, Ap Sequence 2310, App Sequence 2436, App Sequence 2436, App Sequence 2436, App Sequence 310, App Sequence 63, App Sequence 64, App Sequence 12372, A Sequence 63, App Sequence 12372, Ap Sequence 12372, Ap Sequence 12372, Ap Sequence 12372, Ap Sequence 1436, App Sequence 715, App Sequence 715, App Sequence 715, App Sequence 71237, App Sequence 71237, App

US-09-796-692-1696
US-09-796-692-2250
US-10-040-862-1239
4 US-10-040-862-1239
4 US-10-040-862-1239
5 US-10-040-862-1239
5 US-10-057-475B-1239
5 US-10-057-475B-1239
5 US-10-057-475B-1239
5 US-10-057-475B-1239
6 US-10-154-884B-1250
6 US-10-154-884B-1239
6 US-10-154-884B-1239
6 US-10-154-884B-1239
6 US-10-154-884B-1239
6 US-10-154-884B-1239
6 US-10-164-324-1696
6 US-10-764-324-1696
6 US-10-764-324-1696
6 US-10-764-324-1696
7 US-10-205-194-93
7 US-10-205-194-93
7 US-10-205-194-93
7 US-10-205-311-94
7 US-10-369-493-12372
7 US-10-369-493-12372
7 US-10-322-281-63

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   April 8, 2005, 10:53:18; Search time 42.6667 Seconds (without alignments) 116.718 Million cell updates/sec
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(ganz 6/ptodata1//pubpaa/US07 PUBCCMB.pep:*
(cgnz 6/ptodata1//pubpaa/US07 PUBCCMB.pep:*
(cgnz 6/ptodata1//pubpaa/US06 PUBF PUB.pep:*
(cgnz 6/ptodata1//pubpaa/US06 PUBCOMB.pep:*
(cgnz 6/ptodata1//pubpaa/US07 NEW PUB.pep:*
(cgnz 6/ptodata1//pubpaa/US08 PUBCOMB.pep:*
(cgnz 6/ptodata1//pubpaa/US09 PUBCOMB.pep:*
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(cgnz 6/ptodata1//pubpaa/US10P_PUBCOMB.pep:*
(cgnz 6/ptodata1//pubpaa/US00-NEW PUB.pep:*
                GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                1418010 segs, 331997259 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                           OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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1 LASLSTFQQMWISKQ 15
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Maximum DB seq length: 200000000
                           Copyright
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Perfect score:
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ALIGNMENTS

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	Description	Sequence 139, App	Sequence 33598, A	Sequence 157586,	Sequence 55472, A	Sequence 4060, Ap	Sequence 2183, Ap	Sequence 2183, Ap	Sequence 2183, Ap	Sequence 2183, Ap	Sequence 2183, Ap	Sequence 143033,	Sequence 4259, Ap	Sequence 1239, Ap
2000	ΩI	US-10-341-434-139	US-10-767-701-33598	US-10-424-599-157586	US-10-767-701-55472	US-10-264-049-4060	US-09-796-692-2183	US-10-040-862-2183	US-10-057-475B-2183	US-10-154-884B-2183	US-10-764-324-2183	US-10-424-599-143033	US-10-264-049-4259	US-09-796-692-1239
	DB	15	16	15	16	15	σ	14	15	15	16	15	15	6
	% Query Match Length DB	47	74	81	95	110	129	129	129	129	129	133	145	147
	& Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
	Score	75	75	75	75	75	75	75	75	75	75	75	75	75
	Result No.	н	7	٣	4	ស	9	7	80	6	10	11	12	13

TITLE OF INVENTED FILE REFERENCE CURRENT APPLICATION OF PRIOR FILING DEVINOR PRIOR FILING DEVINOR PRIOR FILING DEVINOR FILING FILING DEVINOR FILING F	TITLE OF INVENTION: Differentially Regulated Prostate Cancer Genes FLIE REFERENCE: 91 204 205 R1 CURRENT APPLICATION NUMBER: 105/10/341,434 CURRENT FILING DATE: 2003-07-18 PRIOR PELICATION NUMBER: US 60/348,164 PRIOR APPLICATION NUMBER: US 60/348,119 PRIOR FILING DATE: 2002-01-15 PRIOR FILING DATE: 2002-01-15 NUMBER OF SEQ ID NOS: 238 SOFTWARE: PatentIN version 3.1 EQ ID NO 139 LENGTH: 47 TYPE: PRT CREANISM: Homo sapiens 10-341-434-139
Query Match Best Local Matches 1	Query Match Best Local Similarity 100.0%; Pred. No. 2.8e-05; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps
٥٨	1 LASLSTROQMWISKQ 15
QQ	18 LASLSTFOOMWISKQ 32

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US-09-796-622-2183

US-09-796-622-2183

Sequence 2183, Application US/09796692

Publication No. US20020198362A1

GENERAL INFORMATION:
GENERAL INFORMATION:
THE CAPPLICANT: Gaiger, Alexander

APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY

TITLE OF INVENTION: COMPOSITION OF COMPOSITION OF COMPOSITION OF COMPOSITION OF COURSENT APPLICATION NUMBER: 60/196,692

CURRENT APPLICATION NUMBER: 60/196,126

FRIOR FILING DATE: 2000-03-01

PRIOR APPLICATION NUMBER: 60/190,479

PRIOR FILING DATE: 2000-04-27

PRIOR APPLICATION NUMBER: 60/200,303

PRIOR FILING DATE: 2000-04-28

PRIOR PRIOR FILING DATE: 2000-04-28

PRIOR APPLICATION NUMBER: 60/200,303

PRIOR FILING DATE: 2000-04-28

PRIOR APPLICATION NUMBER: 60/200,999

PRIOR PRILING DATE: 2000-05-01

PRIOR APPLICATION NUMBER: 60/200,999

PRIOR APPLICATION NUMBER: 60/200,999
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PAI33P1
CURRENT APPLICATION NUMBER: US/10/264,049
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: PCT/US01/18569
PRIOR FILING DATE: 2001-06-07
PRIOR FILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 4360
                                                                                                                                                                                                                                                                                                                                                               Indels
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Pred. No. 5.6e-05;
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Best Local Similarity 100.0%; Pred. No. 6.4e-05;
Matches 15; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                    FEATURE:

OTHER INFORMATION: Clone ID: 30163357.pep
US-10-767-701-55472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 4060, Application US/10264049; Publication No. US20040005579A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                            Query Match
100.0%; Some Sest Local Similarity 100.0%; Prometions 15; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         66 LASLSTFOOMWISKO 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Ver. 3.1
SEQ ID NO 4060
                                                                                                                                                           TYPE: PRT
ORGANISM: Sorghum bicolor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Homo sapiens
US-10-264-049-4060
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ABPLICANT: Zhou, Yihua

APPLICANT: Zhou, Yihua

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

FILE REFREENCE: 38-21(53535) B

CURRENT APPLICATION NUMBER: US/10/767,701

CURRENT FILING DATE: 2004-01-29

NUMBER OF SEQ ID NOS: 63128

SEQ ID NO 33598

LENGTH: 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 157566, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: La Rosa Thomas J
APPLICANT: Easo Thomas J
APPLICANT: About K
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
SEQ ID NOS: 285684
SEQ ID NO 157886
LENGTH: 81
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Sequence 55472, Application US/10767701

Sequence 55472, Application US2040172684A1

Sequence 55472, Application NUS2040172684A1

GENERAL INFORMATION:

APPLICANT: Kovalic, David K.

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

FILE REFERENCE: 38-21(53535)8

CURRENT APPLICATION NUMBER: US/10/767,701

CURRENT FILING DATE: 2004-01-29

NUMBER OF SEQ ID NOS: 63128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C33956_1.pep
US-10-767-701-33598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Clone ID: PAT_MRT3847_11331C.1.pep
US-10-424-599-157586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 75; DB 16;
Pred. No. 4.4e-05;
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Best Local Similarity 100.0%;
Matches 15; Conservative 0.
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Best Local Similarity 100.00
Thes 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Sorghum bicolor
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APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Mannion, Jane
APPLICANT: Clapper, Jonathan David
APPLICANT: Clapper, Jonathan David
APPLICANT: Ordonez, Nadia
APPLICANT: Carter, Lauren
APPLICANT: Carter, Lauren
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
TITLE OF INVENTION: Hematological Malignancies
FILE REFERENCE: 014056-014402US
CURRENT APPLICATION NUMBER: US/10/057,475B
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PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR FILING DATE: 2000-03-01
PRIOR FILING DATE: 2000-03-17
PRIOR PLICATION NUMBER: US 60/200,545
PRIOR PLIING DATE: 2000-04-27
PRIOR PLIING DATE: 2000-04-28
PRIOR PLIING DATE: 2000-04-28
PRIOR PLIING DATE: 2000-04-28
PRIOR PLIING DATE: 2000-05-01
PRIOR PLIING DATE: 2000-05-01
PRIOR PLIING DATE: 2000-05-01
PRIOR PLIING DATE: 2000-05-01
PRIOR FILING DATE: 2000-05-01
PRIOR FILING DATE: 2000-05-01
PRIOR FILING DATE: 2000-05-04
PRIOR PLING DATE: 2000-05-22
PRIOR PLING DATE: 2000-05-22
PRIOR PLING DATE: 2000-05-24
PRIOR PLING DATE: 2000-06-22
PRIOR PLING DATE: 2000-06-23
PRIOR PLING DATE: 2000-06-23
PRIOR PLING DATE: 2000-06-23
PRIOR PLING DATE: 2000-06-32
PRIOR PLING DATE: 2000-06-33
PRIOR PLING DATE: 2000-06-32
PRIOR PLING DATE: 2000-06-32
PRIOR PLING DATE: 2000-06-33
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Pred. No. 7.5e-05;
; Mismatches 0; Indels (
NUMBER OF SEQ ID NOS: 10467
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2183
LENGTH: 129
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; OTHER INFORMATION: Xaa = Any amino acid
US-10-057-475B-2183
                                                                                                                                                                                                                                                     NAME/KEY: variant
COCATION: (1)...(129)
OTHER INFORMATION: Xaa = Any amino acid
US-10-040-862-2183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2183, Application US/10057475B Publication No. US20040002068A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ·;
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Best Local Similarity 100.0%;

Matches 15; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 LASLSTFOOMWISKO 15
                                                                                                                                                                                ORGANISM: Homo sapiens
FEATURE:
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                                                                                                                                                 TYPE: PRT
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APPLICANT: Algaer, Paul A.
APPLICANT: Algaer, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Mannion, Jane
APPLICANT: Retter, Marc
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
TITLE OF INVENTION: Hematological Malignancies
TITLE OF INVENTION: UNBER: US 10/10/040,862
CURRENT APPLICATION NUMBER: US 60/126,126
PRIOR APPLICATION NUMBER: US 60/120,479
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR APPLICATION NUMBER: US 60/200,303
PRIOR APPLICATION NUMBER: US 60/200,779
PRIOR APPLICATION NUMBER: US 60/200,779
PRIOR APPLICATION NUMBER: US 60/200,799
PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR PILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,094
PRIOR PILING DATE: 2000-04-28
PRIOR PILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: US 60/200,094
PRIOR FILING DATE: 2000-05-04
PRIOR FILING DATE: 2000-05-04
PRIOR PILING DATE: 2000-05-04
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100.0%; Pred. No. 7.5e-05;
tive 0; Mismatches 0;
                              PRIOR APPLICATION NUMBER: 60/206,201
PRIOR PLING DATE: 2000-05-22
PRIOR PLING DATE: 2000-05-22
PRIOR PLING DATE: 2000-07-14
PRIOR PILING DATE: 2000-07-14
PRIOR PILING DATE: 2000-08-03
PRIOR PILING DATE: 2000-08-04
PRIOR PILING DATE: 2000-08-07
NUMBER OF SEQ ID NOS: 9597
SOFTWARE: PESESEQ for Windows Version 3.0
SEQ ID NO 2183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: variant
CACATION: (1)...(129)
COTHER INFORMATION: Xaa = Any amino acid
WS-09-796-692-2183
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APPLICATION NUMBER: US 60/223,378
ELLING DATE: 2000-08-07
APPLICATION NUMBER: US 09/796,692
PILING DATE: 2001-03-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2183, Application US/10040862
Publication No. US20030078396A1
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   FILING DATE: 2000-05-04
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APPLICANT: Gaiger, Alexander
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
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APPLICANT: Retter, Marc
APPLICANT: Retter, Marc
APPLICANT: Retter, Marc
APPLICANT: Coriva Corporation
ITILE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy,
ITILE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy,
ITILE OF INVENTION: Hematological Malignancies
FILE REFERENCE: 014058-01352005
CURRENT APPLICATION NUMBER: US/10/764,324
CURRENT FILING DATE: 2004-01-23
PRIOR FILING DATE: 2000-03-01
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR PELICATION NUMBER: US 60/200,545
PRIOR PELICATION NUMBER: US 60/200,709
PRIOR PELICATION NUMBER: US 60/200,709
PRIOR PELICATION NUMBER: US 60/200,709
PRIOR PELICATION NUMBER: US 60/200,909
PRIOR PELICATION NUMBER: US 60/200,909
PRIOR PELICATION NUMBER: US 60/200,909
PRIOR PELICATION NUMBER: US 60/200,009
PRIOR PELICATION NUMBER: US 60/200,
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APPLICANT: La Rosa Thomas J
APPLICANT: Exovalic David K
APPLICANT: Should R
APPLICANT: About Thus
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/424, 599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
LENGTH: 133
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US-10-424-599-143033
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NOMEN(FEX: variant.
LOCATION: (1)...(129)
OTHER INFORMATION: Xaa = Any amino acid
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Publication No. US20040031072A1
GENERAL INFORMATION:
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Best Local Similarity 100.u
...hes 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
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ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-424-599-143033
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LENGTH: 129
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                                                                                                                                                                                                                                                                                                                                                                                                             PAPLICANT: Algate 2183, Application US/10154804B
| Publication No. US20040005561A1
| GENERAL INFORMATION:
| APPLICANT: Gaiger, Alexander APPLICANT: Reter, Warc W.
| APPLICANT: Conjustions and Methods for the Detection, Diagnosis and Therapy.
| TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy.
| TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy.
| TITLE OF INVENTION: Hematological Malignancies
| TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy.
| TITLE OF INVENTION: Hematological Malignancies
| TITLE OF INVENTION: HEMBER: US 60/190, 479
| PRIOR FILING DATE: 2000-04-28
| PRIOR PILING DATE: 2000-04-28
| PRIOR PELING DATE: 2000-04-28
| PRIOR PELICATION NUMBER: US 60/200, 999
| PRIOR PILING DATE: 2000-06-30
| PRIOR PILING DATE: 2000-06-30
| PRIOR PILING DATE: 2000-06-30
| PRIOR FILING DATE: 2000-06-30
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Query Match

100.0%; Score 75; DB 15; Length 129;
Best Local Similarity 100.0%; Pred. No. 7.5e-05;
Matches 15; Conservative 0; Mismatches 0; Indels
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                                                                                      Indels
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; OTHER INFORMATION: Xaa = Any amino acid
US-10-154-8848-2183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2183, Application US/10764324
Publication No. US20040175739A1
GENERAL INFORMATION:
APPLICANT: Galger, Alexander
APPLICANT: Algate, Paul A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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                                                                                                                                                               1 LASLSTFOOMWISKO 15
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Best Local Similarity 100.
Matches 15; Conservative
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US-10-764-324-2183
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Gaps

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APPLICANT: Adgate, Paul A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
FILE REPERENCE: 2077 -001200
CURRENT APPLICATION NUMBER: 60/190,479
PRIOR PILING DATE: 2000-03-17
PRIOR PILING DATE: 2000-04-17
PRIOR PILING DATE: 2000-04-28
PRIOR PILING DATE: 2000-04-28
PRIOR PILING DATE: 2000-04-28
PRIOR PILING DATE: 2000-05-01
PRIOR PILING DATE: 2000-08-04

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; Pred. No. 8.5e-05;
0; Mismatches 0; Indels
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100.0%; Pred. No. 8.5e-05;
tive 0; Mismatches 0;
       PRIOR FILING DATE: 2000-07-14

FRICH RIGHT APPLICATION NUMBER: 60/222,903

PRIOR FILING DATE: 2000-08-03

PRIOR FILING DATE: 2000-08-03

PRIOR FILING DATE: 2000-08-04

PRIOR PILING DATE: 2000-08-04

PRIOR PILING DATE: 2000-08-07

NUMBER: 60/223,378

PRIOR PILING DATE: 2000-08-07

NUMBER OF SEQ ID NOS: 9597

SEQ ID NO 1239

LENGTH: 147
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   60/218,950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       118 LASLSTFOOMWISKO 132
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ilarity 100.0%;
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Best Local Similarity 100.0
....hem 15; Conservative
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; ORGANISM: Homo sapiens
US-09-796-692-1239
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US-09-796-692-1696
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Best Local Simil
Matches 15; (
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Sequence 1239, Application US/09796692

Publication No. US20020198362A1

GENERAL INCRMATION:

APPLICANT: Gaiger, Alexander

APPLICANT: Algate, Paul A.

APPLICANT: Algate, Paul A.

APPLICANT: Mannion, Jane

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY

TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES

TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES

FILE REFERENCE: 2077.001200

CURRENT FILING DATE: 2001-03-01

PRIOR PLLING DATE: 2000-03-01

PRIOR PLLING DATE: 2000-04-27

PRIOR PLLING DATE: 2000-04-28

PRIOR APPLICATION NUMBER: 60/200, 779

PRIOR PLLING DATE: 2000-06-08

PRIOR PLLING DATE: 2000-06-09

PRIOR PLLING DATE: 2000-06-01

PRIOR PLLING DATE: 2000-06-01
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. OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids US-10-264-049-4259
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Publication No. US2004000557941

GENERAL INFORMATION:

APPLICANT: Birse et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REPERENCE: PA13791

CURRENT FILING DATE: 2002-10-04

PRIOR APPLICATION NUMBER: PCT/US01/18569

PRIOR APPLICATION NUMBER: PCT/US01/18569

PRIOR PILING DATE: 2001-06-07

PRIOR FILING DATE: 2000-06-07

PRIOR FILING DATE: 2000-06-07

PRIOR FILING DATE: 2000-06-07

PRIOR FILING DATE: 2000-06-07

SOFTWARE: PLENGTH: NOS: 4360

SOFTWARE: PLENGTH: 145
100.0%; Score 75; DB 15; Length 133; 100.0%; Pred. No. 7.7e-05;
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                                                                    0; Mismatches
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FILING DATE: 2000-05-22
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                                                                                                                                         1 LASLSTFOOMWISKQ 15
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Matches 15; Conservative
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ORGANISM: Homo sapiens
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                            Best Local Similarity
Matches 15; Conserv
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US-10-264-049-4259
   Query Match
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100.0%; Score 75; DB 9; I
Best Local Similarity 100.0%; Pred. No. 8.5e-05;
Matches 15; Conservative 0; Mismatches 0;
                                                      118 LASLSTFOOMWISKO 132
1 LASLSTFOOMWISKO 15
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CORGANISM: Homo sapiens
US-09-796-692-2250
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Search completed: April 8, 2005, 12:51:00 Job time : 43.6667 secs

118 LASLSTFOOMWISKO 132

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ADDRESSEE: McGregor & Adler,
STREET: 8011 Candle Lane
CITY: Houston
STATE: Texas
COUNTRY: USA
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Matches 15; Conservative
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                                                 NAME/KEY: UNSURE
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9424, Ap
10757, A
11313, A
14109, A
3, Appli
2, Appli
5, Appli
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Sequence 6, Appli
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Sequence 16, Appl
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                                                                                                                                                                             8, 2005, 09:58:57; Search time 17.5333 Seconds (without alignments) 63.863 Million cell updates/sec
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
                        GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-09-611-022-7
US-09-976-594-731
US-09-976-594-731
US-09-949-016-6100
US-09-106-217-2
US-09-117-233
US-09-919-1172-33
US-09-949-016-7721
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US-09-538-092-1110
US-09-949-016-6656
US-09-949-016-8452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -09-171-337A-7
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                              - protein search, using sw model
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Maximum DB seq length: 200000000
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Match Length
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377
377
386
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402
377
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                                                                                                                                                                                                                                                                                                                                                                                                   Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Perfect score:
                                                                                                                                 OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Database :
                                                                                                                                                                                                                                                                                                                                                  Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Searched:
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Sequence 10, Appl
Sequence 6655, Ap
Sequence 7396, Ap
Sequence 28810, A
Sequence 11948, A
Sequence 11948, A
Sequence 25373, A
Sequence 5181, Ap
Sequence 5181, Ap
Sequence 5181, Ap
   Sequence 1
Sequence 1
Sequence 6
                                                                                                                                                                                                                                                             Sequence 2
Sequence 2
Sequence 2
US-08-505-250-17

US-09-554-7266-10

US-09-949-016-7396

US-09-949-016-7396

US-09-252-9104-28830

US-09-502-540-11948

US-09-518-090-1142

US-09-518-090-1142

US-09-522-991A-25373

US-09-252-991A-16880

US-09-252-991A-16880

US-09-252-991A-26312

US-09-252-991A-26312

US-09-252-991A-26312

US-09-252-991A-26312

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US-09-252-991A-26312

US-09-252-991A-26312

US-09-252-991A-26312
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Gaps
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US-08-609-236-6
US-08-609-236-6
Sequence 6, Application US/08609236
Patent No. 6087398
GENERAL INFORMATION:
TATLLE OF INVENTON: No. 6087398el Sickle Cell Anemia Treatment
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 71;
Sequence 6521, Application US/09621976

Patent No. 6639063

GENERAL INPORMATION:
APPLICANT: Johert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION ESTE and Encoded Human Proteins.
FILE REFERENCE: GENSET. 054PR2
CURRENT APPLICANT NONEXTION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SEQ ID NO 6521
LENGTH: 71
LENGTH: 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 80; DB 4; I 100.0%; Pred. No. 9.4e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                               LOCATION: 62
OTHER INFORMATION: Xaa = Ala,Ser
NAME/KEY: UNSURE
                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Xaa = Leu,Val
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Keating, Mark T.

APPLICANT: Olson, Timothy M.

TITLE OF INVENTION: Actin Mutations in Dilated

TITLE OF INVENTION: Cardiomyopathy, a Heritable Form of Heart Failure
NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.

STREET: 555 Thirteenth Street, N.W., Suite 701 East

STREET: Gover

CITY: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 80; DB 2; Length 375; 100.0%; Pred. No. 5.7e-06; Live 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin.Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/106,217
                                    NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REGISTRATION NUMBER: 29,659
REPERENCE/DOCKET NUMBER: 24615-20039.01
TELECOMMUNICATION INFORMATION:
TELEPRONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-106-217-16
; Sequence 16, Application US/09106217
; Patent No. 6063576
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NAME: Saxe, Stephen A.

REGISTRATION UNDERE: 2323-
REFERENCE/DOCKET UNDERE: 2323-
TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-783-6040
TELEPAX: 202-783-6040
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 APRAVFPSIVGRPRH 15
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          ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: DC COUNTRY: U.S.A. ZIP: 20004 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-494-151-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein US-09-106-217-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/494,151
FILING DATE: 23-JUN-1995
CLASSIPICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
100.0%; Score 80; DB 3; I
Best Local Similarity 100.0%; Pred. No. 5.7e-06;
Matches 15; Conservative 0; Mismatches 0;
COMPUTER READBLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word for Macintosh
SOFTWARE: Microsoft Word for Macintosh
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/609,236
FLING DATE: March 1, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/002,288
FLING DATE: August 14, 1995
CLASSIFICATION: 514
ATTORNEY/AGENT INPORMATION:
NAME: Benjamin Aaron Adler, Ph.D.
REGISTRATION NUMBER: 35,423
REFERENCE/POCKET NUMBER: D5807
TELECOMMUTCATION INFORMATION:
TELEPHONE: 713-777-2231
TELEFRA: 713-777-2231
TELEFRA: 713-777-2231
TELEFRA: 713-777-2231
SUNFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYBE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SYSTEM: PC-DOS/MS-DOS
SYSTEM: PATENTINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 APRAVFPSIVGRPRH 15
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MOLECULE TYPE:
DESCRIPTION: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: Amino acid
STRANDEDNESS:
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
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Gaps
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ZIP: 10023
COMPUTER: BADABLE FORM:
MEDIUM TYPE: 3-1/4" Disk 1.44MB
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Microsoft Windows
SOFTWARE: Worderfect 8 for Windows
SOFTWARE: Worderfect 8 for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/171,337A
FILING DATE: 14-May-1999
CLASSIFICATION S36
PRIOR APPLICATION NUMBER: PCT/ES98/00056
PILING DATE: S-MAR-1998
APPLICATION NUMBER: ES9700482
FILING DATE: S-MAR-1997
ATTORNEY/AGENT INFORMATION:
MAME: MASS, Clifford J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: amino acid sequence of the -actin protein with a molecular weight of
                                                                                                                                                                                                                     DESHYDROGENASE, -N.ACETYLHEXOSAMINIDASE
AND -ACTIN AND THEIR USE IN FILAMENTOUS
FUNGI EXPRESSION, SECRETION AND ANTISENSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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                                                                                                                                                   SALTO MALDONADO, Francisco
DIEZ GARCIA, Bruno
TITLE OF INVENTION: PROMOTERS OF THE GENES GLUTAMATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REF. / DOCKET NO.:
                                                           APPLICANT: BARREDO FUENTE, Jose Luis
RODRIGUEZ SAIZ, Marta
COLLADOS DE LA VIEJA, Alfonso J.
MORENO VALLE,Migeul Angel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Acremonium chrysogenum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7, Application US/09631022
Patent No. 6558921
GENERAL INFORMATION:
APPLICANT: BARREDO FUENTE, JOSE Luis
RODRIGUEZ SAIZ, Marta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41612 Da.
SEQUENCE DESCRIPTION: SEQ ID NO: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 30,086
                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: LADAS & PARRY
STREET: 26 WEST 61 STREET
CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 233288
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acids
Sequence 8, Application US/09171337A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.
Matches 15; Conservative
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US-09-631-022-7
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US-09-171-337A-8

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Sequence 731, Application US/09976594

Patent No. 6673549

GENERAL INFORMATION:
APPLICANT: Furness, Michael
APPLICANT: Buchbinder, Jenny
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
FILE REPERBNCE: PA-0041 US
CURRENT FILLING DATE: 2001-10-12
PRIOR PILING DATE: 2000-10-12
PRIOR FILING DATE: 2000-10-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-976-594-731
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                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: 3-14" Disk 1.44MB
COMPUTER: IBW PC compatible
OPERATING SYSTEM: Microsoft Windows
OPERATING SYSTEM: Microsoft Windows
SOFTWARE: Wordberfect 8 for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/631,022
FILING DATE: 02-Aug-2000
CLASSIFICATION: 536
PRIOR APPLICATION NUMBER: 09/171,337
FILING DATE: 14-MAY-1999
APPLICATION NUMBER: PCT/RS98/00056
FILING DATE: 5-MAR-1998
APPLICATION NUMBER: ES9700482
FILING DATE: 5-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: NAAS, Clifford J.
REGISTRATION NUMBER: 30,086
REGISTRATION NUMBER: 30,086
COLLADOS DE LA VIEJA, Alfonso J.
MORENO VALLE, Migeul Angel
SALOR MALDONADO, Francisco
DIEZ GARCIA, Bruno
TITLE OF INVENTION: PROMOTERS OF THE GENES GLUTAMATE
DESHYDROGHASE, -N-ACETYLHEXOSAMINIDASE
AND -ACTIM AND THEIR USE IN FILAMENTOUS
FUNGI EXPRESSION, SECRETION AND ANTISENSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: amino acid sequence of the -actin protein with a molecular weight of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REF./DOCKET NO.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.7e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 8, Application US/09631022
Patent No. 6558921
GENERAL INFORMATION:
APPLICANT: BARREDO FUENTE, Jose Luis
RODRIGUEZ SAIZ, Marta
RODRIGUEZ SAIZ, Marta
RODRIGUEZ SAIZ, Marta
MORENO VALLE, MIGGUI AUGEI
SALTO MALDONADO, Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 80; DB
100.0%; Pred. No. 5.7
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Penicillium chrysogenum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE DESCRIPTION: SEQ ID NO: 7
US-09-631-022-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 375 amino acide
TYPE: amino acide
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 233288
INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                 ADDRESSEE: LADAS & STREET: 26 WEST 61
                                                                                                                                                                                                                                                                                                                                       ZIP: 10023
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 APRAVFPSIVGRPRH 15
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                                                                                                                                                                                    NUMBER OF SEQUENCES: 20 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0
Matches 15; Conservative
                                                                                                                                                                                                                                                                         CITY: NEW YORK
STATE: NY
                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 8
US-09-631-022-8
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COMPUTER: IBM PC compatible
COMPUTER: Maicrosoft Windows
SOFTWARE: Worderfect 8 for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/631,022
FILING DATE: 02-Aug-2000
CLASSIFICATION NUMBER: 09/171,337
FILING DATE: 14-MAX-1999
APPLICATION NUMBER: PCT/ES98/00056
FILING DATE: 5-MAX-1998
APPLICATION NUMBER: S9700482
FILING DATE: 5-MAR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                 AND -ACTIN AND THEIR USE IN .....FUNGI EXPRESSION, SECRETION AND ANTISENSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -actin
DIEZ GARCIA, Bruno
TITLE OF INVENTION: PROMOTERS OF THE GENES GLUTAMATE
DESHYDROGENASE, -N-ACETYLHEXOSAMINIDASE
AND -ACTIN AND THEIR USE IN FILAMENTOUS
AND -ACTIN AND THEIR SEES IN FLAMENTOUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OLINEX INFURMATION: amino acid sequence of the protein with a molecular weight of 41612 na
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REF./DOCKET NO.:
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100.0%; Pred. No. 5.7e-06;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: Peptide
ORIGINES: Peptide
ORGANISM: Acremonium chrysogenum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; $\frac{41612}{41612}Da.$; $\frac{1}{1000}SEQUENCE DESCRIPTION: SEQ ID NO: 8 US-09-631-022-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: MASS, Clifford J. REGISTRATION NUMBER: 30,086
                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: LADAS & PARRY
STREET: 26 WEST 61 STREET
CITY: NEW YORK
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 233288
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHRACTERISTICS:
IENGTH: 375 amino acids
TYPE: amino acids
STRANDEDNESS: single
                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 10023
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 APRAVFPSIVGRPRH 15
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                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 15; Conservative
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; MOLECULE TYPE: protein US-09-106-217-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-949-016-6100
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US-09-106-217-2
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                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 80; DB 4; Length 375; Best Local Similarity 100.0%; Pred. No. 5.7e-06; Matches 15; Conservative 0; Mismatches 0; Indels
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; Pred. No. 5.7e-06;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT:
ACHORN, KIRK M.
TITLE OF INVENTION: DIAGNOSTIC TEST FOR DETERMINING
TITLE OF INVENTION: MALIGNANCY OF SMOOTH MUSCLE TUMORS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
ADDRESSEE: Woodcock Washburn Kurtz Packiewicz &
ADDRESSEE: Woodcock Washburn Fackiewicz &
ADDRESSEE: Woodcock Washbu
                                                                                                                                                                                                                          ; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 1837317CD1
US-09-976-594-731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 19103

ZIP: 19103

MEDIUM TYER FORM:
MEDIUM TYER Floppy disk
COMPUTER: Floppy disk
COMPUTER: PROPERTIBLE
COMPUTER: PACHOLINE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/588,113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Ralph, Rebecca L.
REGISTRATION NUMBER: 35,152
REFERENCE/DOCKET NUMBER: TJU-1652
TELECOMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 376 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08588113
Patent No. 5710003
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Best Local Similarity 100.
Matches 15; Conservative
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NUMBER OF SEQ ID NOS: 1143
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                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
                                   SOFTWARE: PERL Program
SEQ ID NO 731
LENGTH: 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 11
US-09-949-016-6100
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US-08-588-113-2
                                                                                                                                                                                                                      FEATURE:
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Sequence 7721, Application US/09949016

Patent No. 681239

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION: WINDER: US/09/949,016

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR PLILNG DATE: 2000-10-20

PRIOR PLILNG DATE: 2000-10-03

SEQ ID NOS: 207012

SEQ ID NO 7721

LENGTH: 386
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Best Local Similarity 100.
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-949-016-7721
            US-09-949-016-7721
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                                                                                              Gaps
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US-09-917-254-53
is Sequence 53, Application US/09917254
is Patent No. 6703204
is GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Muter, George
is APPLICANT: Baak, Jan
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/09/917,254
CURRENT APPLICATION NUMBER: US/09/917,254
is FRIOR FILING DATE: 2001-07-28
is NUMBER OF SEQ ID NOS: 102
is SOFTWARE: PatentIn version 3.0
is SEQ ID NO 53
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Query Match 100.0%; Score 80; DB 3; Length 377; Best Local Similarity 100.0%; Pred. No. 5.7e-06; Matches 15; Conservative 0; Mismatches 0; Indels
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; OTHER INFORMATION: Incyte ID No. 6673545 1709118CD1
US-09-919-172-33
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 33, Application US/09919172
| Sequence 33, Application US/09919172
| Patent No. 6673545
| GENERAL INFORMATION:
| APPLICANT: Faris, Mary
| APPLICANT: Turner, Christopher M.
| TITLE OF INVENTION: PROSTATE CANCER MARKERS
| FILE REPERBNES: PA-0036 US
| CURRENT APPLICATION NUMBER: US/09/919,172
| CURRENT FILING DATE: 2001-07-30
| PRIOR PAPLICATION NUMBER: 60/222,469
| NUMBER OF SEQ ID NOS: 102
| SOFTWARE: PERL PROGram
| SEQ ID NO 33
| LEMOTH: 377
| TYPE: PRI
                                                                                                                                                            1 APRAVFPSIVGRPRH 15
                                                                                                                                                                                                                                      28 APRAVFPSIVGRPRH 42
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CORGANISM: Homo Sapiens
US-09-917-254-53
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Best Local Similarity
Matches 15; Conserva
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à g RESULT 15

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Gaps

; 0

0; Indels

0; Mismatches

Jeguence 64, Appl Sequence 162009, Sequence 122816, Sequence 223492, Sequence 28331

Sequence 198295,

Sequence Sequence

Sequence Sequence Sequence

ALIGNMENTS

Sequence Sequence

Sequence 6 Sequence 4 Sequence 1

Sequence 202420, Sequence 45677, A Sequence 46090, A Sequence 33, Appl Sequence 52, Appl Sequence 64, Appl

Sequence 101, App Sequence 179917,

Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Descriptions

US-10-205-194-93 US-10-316-253-88 US-10-369-493-1786 US-10-369-493-5927 US-10-369-493-5927 US-10-205-331-94 US-10-205-331-94 US-10-361-434-101 US-10-341-434-101 US-10-437-963-202420 US-10-437-963-202420 US-10-437-963-202420 US-10-767-701-46090

Sequence

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NAME/KEY: MISC_FEATURE

1 LOCATION: (103)

2 OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids

US-10-264-049-3601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3601, Application US/10264049
; Publication No. US20040005579A1
; BENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INNENTION: Nucleic Acids, Proteins, and Antibodies
; TITLE OF INNENTION: Nucleic Acids, Proteins, and Antibodies
; TITLE OF INNENTION: Nucleic Acids, Proteins, and Antibodies
; TITLE OF INNENTION: Nucleic Acids, Proteins, and Antibodies
; CURRENT APPLICATION NUMBER: US/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR PILING DATE: 2000-66-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: Patentin Ver. 3.1
; SEQ ID NO 3601
                                                                                                                                                                                                                                                 0.5-10.7-7.11-46.09.0
0.5-10.7-38
0.10-318-77-52
5. US-10-236-0318-64
5. US-10-424-599-162019
5. US-10-424-599-223492
5. US-10-424-599-223492
5. US-10-424-599-283336
5. US-10-424-599-283336
5. US-10-424-599-283336
5. US-10-437-963-198295
0.5-10-437-963-198295
0.5-10-437-963-198295
0.5-10-425-114-59265
0.5-10-425-114-59265
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0.5-10-425-114-59265
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100.0%; Pred. No. 1.7e-05;
iive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 15, Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-264-049-3601
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Sequence 280810,
Sequence 41308, Ap
Sequence 282905,
Sequence 56, Appl
Sequence 56, Appl
Sequence 4008, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3601, Ap
Sequence 47318, A
Sequence 280811,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68, Appl
                                                                                                                                  ; Search time 42.6667 Seconds
(without alignments)
116.718 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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(gnz 6/prodata/1/pubpaa/US07_PUBCOMB.pep:*

(gnz 6/prodata/1/pubpaa/PCT_NEW_PUB.pep:*

(gnz 6/prodata/1/pubpaa/US06_PUBCOMB.pep:*

(gnz 6/prodata/1/pubpaa/US06_PUBCOMB.pep:*

(gnz 6/prodata/1/pubpaa/US06_PUBCOMB.pep:*

(gnz 6/prodata/1/pubpaa/US08_PUBCOMB.pep:*

(gnz 6/prodata/1/pubpaa/US108_PUBCOMB.pep:*

(gnz 6/prodata/1/pubpaa/US108_PUBCOMB.pep:*
              GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-4767-701-47318
US-10-424-599-280811
US-10-424-599-280810
US-10-264-049-4148
US-10-264-049-4148
US-10-002-611C-56
US-10-002-611C-56
US-10-108-260A-4008
US-10-108-260A-4008
US-10-424-599-283333
US-10-322-281-68
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Published Applications AA:*
                                                                                           OM protein - protein search, using sw model
                                                                                                                                    April 8, 2005, 10:53:18
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length DB
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Gaps

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Length 105; Indels

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Sequence 280810, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT:
Cao Yongwei
APPLICANT:
Cao Yongwei
TITLE OF INVENTION:
PILE OF DATE:
2003-04-28
CURRENT FILING DATE:
2003-04-28
NUMBER OF SEQ ID NOS: 285684

ENGINE INFORMATION:
ENGINE INFORMATION:
SEQ ID NO SEQ ID NOS: 2805684
            APPLICANT: Cao Yongwei TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21 (53223) B CURRENT APPLICATION NUMBER: US/10/424,599 CURRENT FILING DATE: 2003-04-28 NUMBER OF SEQ ID NOS: 285684 SEQ ID NO 184471 LENGTH: 142
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; Sequence 4308, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
    APPLICANT: Birse et al.
    TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REPERENCE: PA133P1
; CURRENT APPLICATION NUMBER: US/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR PILING DATE: 2001-06-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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US-10-424-599-280810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 80; DB 15;
Pred. No. 3.2e-05;
); Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (1)..(197)
OTHER INFORMATION: unsure at all Xaa locations
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hes 15; Conservative
                                                                                                                                                                                                                                                        ORGANISM: Glycine max
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Best Local Similarity
Matches 15, Conserv
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                                                                                                                                                                                                                                                                                                                           US-10-424-599-184471
                                                                                                                                                                                                                                    TYPE: PRT
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Sequence 280811, Application US/2040031072A1
Sequence 280811, Application No. US2040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
Cao Yongwei
TITLE OF INVENTION:
Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION:
FILE REFERENCE: 38-21 (5323) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT APLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
       Sequence 47318, Application US/10767701
Publication No. US20040172684A1
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
CURRENT FILIS ESPERIOR: 38-21 (55.535) B
CURRENT FILING DATE: 2004-01-29
KUMBER OF SEQ ID NOS: 63128
SEQ ID NO 47318
ILENGTH: 135
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US-10-424-599-280811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) OTHER INFORMATION: Clone ID: SORBI-28MAY03-C105_2.pep
US-10-767-701-47318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 80; DB 16; Best Local Similarity 100.0%; Pred. No. 2.1e-05; Matches 15; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: unsure
LOCATION: (1)..(135)
OTHER INFORMATION: unsure at all Xaa locations
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; Sequence 184471, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 APRAVFPSIVGRPRH 15
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Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Sorghum bicolor
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US-10-767-701-47318
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and Other Molecules Associated With
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TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(3322)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
SEQ ID NOS: 285684
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APPLICANT: Graff, Jonathon M.
APPLICANT: Muenster, Matthew
TITLE OF INVENTION: METHODS TO IDENTIFY SIGNAL SEQUENCES
FILE REFERENCE: A34943 090495.0243
CURRENT APPLICATION NUMBER: US/10/002,631C
CURRENT APPLICATION NUMBER: 60/1-10-31
PRIOR APPLICATION NUMBER: 60/300,309
PRIOR FILING DATE: 2001-06-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Clone ID: PAT_MRT3847_97486C.1.pep
US-10-424-599-282905
                                                                                                                                                                                                                                                                         Score 80; DB 15;
Pred. No. 3.3e-05;
); Mismatches 0;
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100.0%; Pred. No. 3.4e-05;
tive 0; Mismatches 0;
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LOCATION: (1)..(208)
OTHER INFORMATION: unsure at all Xaa locations
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SOFTWARE: FastSEQ for Windows Version 4.0
PRIOR APPLICATION NUMBER: PCT/US01/18569
PRIOR FILING DATE: 2001-06-07
PRIOR APPLICATION NUMBER: US 60/209,467
PRIOR FILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 4360
SOFTWARE: Patentin Ver. 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 282905, Application US/10424599 Publication No. US20040031072A1
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; Sequence 56, Application US/10002631C
; Publication No. US20030157486A1
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                                                                                                                                                                                                                                                                              100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
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Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                              Query Match 100.
Best Local Similarity 100.
Matches 15, Conservative
                                                                                                                                                                                                           ; ORGANISM: Homo sapiens
US-10-264-049-4148
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ORGANISM: Glycine max
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                                                                                                                                                                   LENGTH: 204
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                                                                                                                                                                                        TYPE: PRT
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OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
                                                                                                                                                                                                                                                           equals any of the twenty naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                equals any of the twenty naturally occurring L-amino acids
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Publication No. US20040005579A1
GENERAL INFORMATION:
APPLICANT: Birse et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PA133P1
CURRENT APPLICANT APPLICATION: NUMBER: US/10/264,049
CURRENT FILING DATE: 2002-10-04
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    PRIOR APPLICATION NUMBER: US 60/209,467
PRIOR FILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 4360
SOFTWARE: PATENTIN VET. 3.1
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                                                                                                                                                                                                                                                        OTHER INFORMATION: Xaa
                                                                                                                                                                                                                                                                                                                                                INFORMATION: Xaa
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                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: MISC FEATURE LOCATION: (140)
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                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: MISC FEATURE
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US-10-264-049-4148
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Best Local S:
Matches 15,
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us-09-423-351c-1.rapb

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GENERAL INFORMATION:
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Sequence 42770, Application US/10767701

Publication No. US20040172684A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
TITLE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUBBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
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                                                                                                          Length 219;
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                                                                                                                                                    Indels
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Publication No. US20040005560A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: No. US20040005560A1e1 full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/10/108,260A
CURRENT APPLICATION NUMBER: US/27
NUMBER OF SEQ ID NOS: 5498
SOFTWARE: Patentin Ver. 2.1
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US-10-767-701-42770
                                                                                                      Query Match
100.0%; Score 80; DB 14;
Best Local Similarity 100.0%; Pred. No. 3.6e-05;
Matches 15; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                      53 APRAVFPSIVGRPRH 67
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Matches 15, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Sorghum bicolor
LENGTH: 219
TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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US-10-767-701-42770
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US-10-108-260A-4008
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                                                              US-10-002-631C-56
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LENGTH: 230
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LENGTH: 342
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RESULT 12

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GENUERCE 283333, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
GENUERAL INFORMATION:
GENUERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
APPLICANT: Cao Yo
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US-10-322-281-68
US-10-322-281-68
Sequence 68, Application US/10322281
Fublication No. US20040126762A1
GENERAL INFORMATION:
APPLICANT: David W. Morris
APPLICANT: Macs S. Malandro
FILE REFRENCE: 529452001000
CURRENT APPLICATION NOWBER: US/10/322,281
SOFTWARE: FREIGN 66
SOFTWARE: FREIGN 66
SOFTWARE: FREIGN 67
SECTION 06
SECTION 06
SECTION 06
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; OTHER INFORMATION; Clone ID: PAT_MRT3847_97873C.1.pep
US-10-424-599-283333
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Pred. No. 5.8e-05;
0; Mismatches 0;
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OTHER INFORMATION: unsure at all Xaa locations
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Publication No. US20030134301A1
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Dixon, Alistair
Brooksbank, Robert
Pinnock, Robert
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Best Local Similarity 100.0%;
Matches 15; Conservative 0
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Best Local Similarity 100.
Matches 15; Conservative
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; ORGANISM: Homo sapiens
US-10-322-281-68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Glycine max
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TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
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100.0%; Score 80; DB 14; Length 375;
Best Local Similarity 100.0%; Pred. No. 6.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
100.0%; Score 80; DB 14; Length 375;
Best Local Similarity 100.0%; Pred. No. 6.3e-05;
Matches 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 15
US-10-316-253-88
Sequence 88, Application US/10316253
Publication No. US20030162706A1
GENERAL INFORMATION
APPLICANT: Thompson, Larry
APPLICANT: Thompson, Larry
APPLICANT: Thompson, Larry
APPLICANT: Thompson, Larry
APPLICANT: Greis, Kenneth
ITLE OF INVENTION: Angiogenesis Modulating Proteins
FILE REFERENCE: 8865M
CURRENT APPLICATION NUMBER: US/10/316,253
CURRENT PILING DATE: 2002-12-10
PRIOR RILING DATE: 2002-12-08
NUMBER OF SEQ ID NOS: 308
SOFTWARE: PatentIn version 3.1
SEQ ID NO 88
LENGTH: 375
FURNAL STATES APPLICATION VIBRES OF SEQ ID NOS: 308
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FURNAL STATES APPLICATION VIBRES APPLICATION SEQ ID 
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                                        FILE REFERENCE: WL-A-018201
CURRENT APPLICATION NUMBER: US/10/205,194
CURRENT FILING DATE: 5200-07-24
FRIOR APPLICATION NUMBER: GB 0118354.0
FRIOR FILING DATE: 2001-07-27
NUMBER OF SEQ ID NOS: 177
SOFTWARE: Patentin Ver. 2.1
SOFTWARE: 375
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; ORGANISM: Rattus norvegicus
US-10-316-253-88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Rattus rattus
FEATURE:
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Search completed: April 8, 2005, 12:50:57 Job time : 43.6667 secs

26 APRAVFPSIVGRPRH 40

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GenCore version 5.1.6
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OM protein - protein search, using sw model

April 8, 2005, 09:58:56 ; Search time 9.3333 Seconds (without alignments) 154.634 Million cell updates/sec Run on:

US-09-423-351C-1 80 1 APRAVFPSIVGRPRH 15 Title: Perfect score:

Scoring table: Sequence:

283416 seqs, 96216763 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:* Database :

1: pirl: * 2: pir2: * 3: pir3: * 4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

DB I	3 2 A43616 actin alpha, cardi	2 C43616 actin	2 A28258 actin 5C - f	2 S03109 actin - pin	2 I49465 alpha-	2 S20097 actin	2 A61043 actin CA15 -	2 A03000	2 S05430 actin	2 T04085 actin - ma	2 A26559	2 A29664 actin - se	1 ATBOB actin beta -		2 JC5818 gamma-a	1 ATBOSM	1 ATRB		Н	1 ATAX actin - Aca	1 ATBY actin - yeast	1 ATCHB actin	1 ATDO actin - slime	1 ATHUB actin	5 1 ATHUG actin gamma 1 - hu	1 ATMSB actin	5 1 ATMSG actin gamma - mous	
% Query Match Length	43	86	137	140	158	195	213	308	328	336	362	370	374	374	374	375	375	375	375	375	375	375	375	375	375	375	375	
% Query Match	100.0	100.0	100.0	100.0	100.0					100.0			100.0	100.0	100.0	100.0	٠.	100.0	100.0	100.0	100.0		100.0	100.0	100.0	100.0		
Score	80	80	80	80	80	80	80	80	80	80	80	80	80	80	80	80	80	80	80	80	80	80	80	80	80	80	80	
Result No.	1	7	9	4	S	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	

actin - yeast (Sac	actin gamma, cytos	actin, cytosolic (	actin gamma - Emer	actin 1 - Pneumocy	hypothetical prote	actin - yeast (Klu	actin - fission ye	actin beta-2, cyto	actin beta-1, cyto	actin beta, cytoso	actin beta - goose	actin alpha, cardi	actin - imperfect	actin - Phaffia rh	actin 7 - fruit fl
JS0702	S11222	533386	JT0385	S47897	T25272	A32798	A26836	S71125	S71124	S71126	A55001	A54728	\$03126	S70377	ATFF7
7	-	N	N	~	N	N	N	~	~	7	~	N	~	~	1
375	375	375	375	375	375	375	375	375	375	375	375	375	375	375	376
100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
80	80	8	80	89	80	80	80	80	80	80	80	80	80	80	80
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

#### ALIGNMENTS

```
RESULT 1
       A43616
```

actin alpha, cardiac - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 16-Jul-1999
C;Accession: A43616
R;Paterson, B.M.; Eldridge, J.D.
R;Paterson, B.M.; Eldridge, J.D.
A;Title: alpha-Cardiac actin is the major sarcomeric isoform expressed in embryonic avia A;Reference number: A43616
A;Reference number: A43616
A;Accession: A43616
A;Accession: A43616
A;Accession: A53616
A;Accession: A53616
A;Accession: A53616
A;Residues: 1-43 cPAT>

A, Cross-references: GB:M10607 C, Superfamily: actin C, Keywords: cardiac muscle; heart

Gaps ö Query Match 100.0%; Score 80; DB 2; Length 43; Best Local Similarity 100.0%; Pred. No. 6.2e-07; Matches 15; Conservative 0; Mismatches 0; Indels

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# 1 APRAVFPSIVGRPRH 15

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## RESULT 2

actin beta, cytosolic - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: ll-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 09-Jul-2004
C;Accession: C45616
R;Paterson, B.M.; Eldridge, J.D.
S;Gience 224, 1436-1438, 1984
A;Title: alhan-Cardiac actin is the major sarcomeric isoform expressed in embryonic avia A;Title: prelimiac actin is the major sarcomeric soform expressed in embryonic avia A;Reference number: A43616; MUID:84223949; PMID:6729461
A;Accession: C45616
A;Accession: C45616
A;Residues: 1-86 cPAT>
A;Residues: 1-86 cPAT>
A;Residues: UNIPROT:Q90736; GB:K02173; NID:g211054; PIDN:AAA98513.1; PID:g211055
C;Superfamily: actin
C;Keywords: cytosol; methylated amino acid
F;73/Modified site: 3'-methylhistidine (His) #status predicted

Gaps ö Query Match 100.0%; Score 80; DB 2; Length 86; Best Local Similarity 100.0%; Pred. No. 1.3e-06; Matches 15; Conservative 0; Mismatches 0; Indels

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## 1 APRAVFPSIVGRPRH 15

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Gaps

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C,Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_cnange Uy-uur-zuu*
C,Accession: A61043
S,Bach, R.L.; Jeffery, W.R.
Dev. Genet. 11, 2-14, 1990
A,Title: Temporal and spatial expression of a cytoskeletal actin gene in the ascidian St
A,Reference number: A61043; MUID:90298580; PMID:2361333
A,Accession: A61043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-195 <DRO>
A;Cross-references: UNIPROT:P30170; EMBL:X55747; NID:g21541; PIDN:CAA39277.1; PID:g13455
C;Genetics:
                                                                                                                          R; Drouin, G.; Dover, G.A.
J. Wol. Evol. 31, 132-150, 1990
A; Title: Independent gene evolution in the potato actin gene family demonstrated by phyl
A; Reference number: S20092; WUID:91012599; PMID:2120451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: not compared with conceptual translation
A;Molecule type: MRNA
A;Residues: 1-213 <BEA>
A;Residues: 1-213 <BEA>
C;Comment: This sequence is expressed in cells undergoing rapid cell division.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Keywords: cytoskeleton; methylated amino acid; mitosis; structural protein F;73/Modified site: 3'-methylhistidine (His) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               actin CA15 - sea squirt (Styela clava) (fragments)
C;Species: Styela clava
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      actin 85c - potato (fragment)
C;Species: Solanum tuberosum (potato)
C;Date: 22-Nov-1993 #sequence_revision 17-Oct-1997 #text_change 09-Jul-2004
C;Accession: S20097
                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:M26776; NID:g191649; PIDN:AAA37166.1; PID:g553859
A;Experimental source: adult cardiac muscle, BALB/c mice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 195;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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100.0%; Pred. No. 2.4e-06;
tive 0; Mismatches 0;
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ilarity 100.0%; Pred. No. 3e-06;
Conservative 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Introns: 132/1
C;Superfamily: actin
C;Keywords: cytoskeleton; structural protein
A;Accession: 149465
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-158 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nilarity 100.0%;
Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Superfamily: actin
C;Keywords: cardiac muscle; heart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 APRAVFPSIVGRPRH 15
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nes 15; Conserv
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nes 15; Conserv
                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 8-158 < RE2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: S20097
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                                                                                                                                                                                                                     C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004
R;Vigoreaux, J.05. Tobin, S.L.
Genes Dev. 1, 116: 1171, 1187
A;Title: Stage-specific selection of alternative transcriptional initiation sites from the A; Reference number: A28258; MUID:88112795; PMID:3123314
A;Recension: A28258
A;Rocession: A28258
A;R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  actin - pin mould (Absidia glauca) (fragment)
C.Species: Absidia glauca
C.Species: Absidia glauca
C.Species: Absidia glauca
C.Species: O7-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C.Accession: 803109
R.Burmester, A.; Weigel, C.; Woestemeyer, J.
R.Burmester, A.; Weigel, C.; Woestemeyer, J.
A.Accession: 803109
A.Accession: 803109
A.Accession: S03109
A.Molecule type: DNA
A.Molecule type: DNA
A.Cross-references: UNIPROT:P10982; EMBL:X07999; NID:g2303; PIDN:CAA30804.1; PID:g578097
A.Introns: 9/3; 31/3
C.Superfamily: actin
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 0.2-011-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: 149466; 149466
R;Garner, I.; Minty, A.J.; Alonso, S.; Barton, P.J.R.; Buckingham, M.B.
EMBO J. 5, 2559-2567, 1996
A;Tile: A 5, Guplication of the alpha-cardiac actin gene in BALB/c mice is associated A;Reference number: 149465; MUID:87053822; PMID:3023046
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Pred. No. 2.1e-06;
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Best Local Similarity 100.0%; Pred. No. 2.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels
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C;Species: Drosophila melanogaster
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Best Local Similarity 100.0%;
Matches 15; Conservative 0
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       26 APRAVFPSIVGRPRH 40
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A;Cross-references: UNIPROT:P93638; EMBL:U60513; NID:g1498392; PIDN:AAB40107.1; PID:g149
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C;Date: 15-Dec-1988 #sequence_revision 30-Sep-1991 #text_change 05-Dec-1997
C;Accession: A29664
R;Crain Jr., W.R.; Boshar, M.F.; Cooper, A.D.; Durica, D.S.; Nagy, A.; Steffen, D. J. Mol. Bvol. 25, 37-45, 1987
Mol. Bvol. 25, 37-45, 1987
A;Title: The sequence of a sea urchin muscle actin gene suggests a gene conversion A;Reference number: A29664; MUID:87311761; PMID:3114500
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C;Species: Gallus gallus (chicken)
C;Species: 09-Sep-1987 #sequence_revision 09-Sep-1987 #text_change 05-Dec-1997
C;Accession: A26559
R;Bergsma, D.J; Chang, K.S.; Schwartz, R.J.
R;Bergsma, D.J; Chang, K.S.; Schwartz, R.J.
A;Reference number: A26559; MUID:85213487; PMID:4000121
                                                                  C;Species: Zea mayĕ (maize)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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A;Residues: 1-370 cCRA-
A;Cross-references: GB:X05739; GB:X05740; GB:X05741; GB:X05742; GB:X05743
A;Note: the authors translated the codon CAG for residue 260 as Glu
                                                                                                                                     C,Accession: T04085
R,de Sa, M.; Drouin, G.
Mol. Biol. Bvol. 13, 1198-1212, 1996
A,Title: Phylogeny and substitution rates of angiosperm actin genes.
A,Reference number: Z15197; MUID:97051711; PMID:8896372
A,Accession: T04085
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C, Superfamily: actin
C, Keywords: cytosol, methylated amino acid
F,74/Modified site: 3'-methylhistidine (His) #status predicted
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C;Keywords: methylated amino acid
F;73/Modified site: 3'-methylhistidine (His) #status predicted
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Pred. No. 5.7e-06;
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                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Superfamily: actin
C;Keywords: cytoskeleton; structural protein
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1 Similarity 100.0%; P
15; Conservative 0;
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Best Local Similarity 100.
Matches 15; Conservative
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Best Local Similarity
Matches 15; Conserv
                                        maize (fragment)
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A; Residues: 1-362 < BER>
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C;Species: Drosophila melanogaster
C;Species: Drosophila: Dro
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C;Species: Ctenopharyngodon idella (grass carp)

C;Species: Ctenopharyngodon idella (grass carp)

C;Species: O'-Jun-1990 #sequence_revision O'-Jun-1990 #text_change 09-Jul-2004

C;Accession: S05430

R;Liu, Z.; Zhu, Z.; Roberg, K.; Faras, A.J.; Guise, K.S.; Kapuscinski, A.R.; Hackett, P. Nucleic Acids Res. 17, 5850, 1989

A;Title: The beta-actin gene of carp (Ctenopharyngodon idella).

A;Reference number: S05430; MUID:89345185; PMID:2762162

A;Reference number: S05430

A;Status: translation not shown

A;Molecule type: DNA

A;References: UNIPROT:P83751; EMBL:M25013

C;Genetics: A;173; 213; 268/1

C;Superfamily: actin

C;Superfamily: actin

C;Keywords: cytoskeleton; methylated amino acid

F;73/Modified site: 3'-methylhistidine (His) #status predicted
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100.0%; Score 80; DB 2; Length 328;
Best Local Similarity 100.0%; Pred. No. 5.2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels
   Length 213;
                                                                      Indels
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Best Local Similarity 100.0%; Pred. No. 4.8e-06;
Matches 15; Conservative 0; Mismatches 0;
100.0%; Score 80; DB 2; I 100.0%; Pred. No. 3.3e-06;
                                                                      0; Mismatches
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Best Local Similarity 100.0
Matches 15, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         actin beta - bovine (tentative sequence)
C;Species: Bos primigenius taurus (cattle)
C;Accession: E14185; A39105; A02999; A14185
C;Accession: E14185; A39105; A02999; A14185
Eur. J Biochem. 90, 451-462, 1978
A;Title: Actin amino-acid sequences. Comparison of actins from calf thymus, bovine brain
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RyVandekerckhove, J.; Weber, K.
Bur. J. Blochem. 90, 421-462, 18-462.
Bur. J. Blochem. 90, 421-462, 18-62.
A.Richte: Actin amino-acid sequences. Comparison of actins from calf thymus, bovine brain A, Reference number: A14185, MUD:79045349; PMID:213279
A, Accession: B14185
A, Accession: B14185
A, Accession: B14185
A, Accessive references: UNIPROT:P02571
A, Residues: 1-374 <VAN>
A, Residues: 1-374 <VAN>
A, Residues: 1-374 <VAN>
A, Residues: action composition from the corresponding peptides of racions of the constant o
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A;Note: only peptides that differed in composition from the corresponding peptides of ra R;Degen, J.L.; Neubauer, M.G.; Degen, S.J.F.; Seyfried, C.E.; Morris, D.R.
J. Biol. Chem. 258, 12153-12162, 1983
A;Title: Regulation of protein synthesis in mitogen-activated bovine lymphocytes. Analys A;Reference number: A39105; MUID:84032385; PMID:6195151
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C;Keywords: blocked amino end; cell motility; cytoskeleton; methylated amino acid; micrd
F;1/Modified site: blocked amino end (Asp) (probably acetylated) #status experimental
F;72/Modified site: 3'-methylhistidine (His) #status predicted
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A;Molecule type: mRNA
A;Residues: 76-227;344-374 <DEG>
A;Esidues: 76-227;344-374 <DEG>
A;Cross-references: GB:K00622; GB:K00623
A;Note: actins beta and gamma were not distinguished in this study
C;Comment: Vertebrate nonmuscle cells contain two highly conserved cytoskeletal actins,
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C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
                                                                                            Gaps
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Query Match 100.0%; Score 80; DB 2; Length 370; Best Local Similarity 100.0%; Pred. No. 5.9e-06; Matches 15; Conservative 0; Mismatches 0; Indels
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Pred. No. 5.9e-06;
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C;Species: Homo sapiens (man)
C;Date: 20-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 09-Jul-2004
C;Date: 20-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 09-Jul-2004
C;Date: 20-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 09-Jul-2004
R;Hauschildt, S.; Schwarz, C.; Heine, H.; Ulmer, A.J.; Flad, H.D.; Rietschel, E.T.; Jens Biochem. Biophys. Res. Commun. 241, 670-674, 1997
A;Title: Actin. A target of lipopolysaccharid-induced phosphorylation in human monocytes A;Accession: JC5818; MUID:98096379; PMID:9414766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: protein
A;Residues: 1-61;84-112;147-190;196-209;215-253;335-358 <HA2>
A;Residues: 1-61;84-112;147-190;196-209;215-253;335-358 <HA2>
B;Experimental source: monocyte
C;Comment: This protein is involved in a signal transduction that eventually leads to more; Superfamily: actin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references: UNIPROT: P02571
A; Experimental source: monocyte
A; Accession: PC4501
                                                                 25 APRAVFPSIVGRPRH 39
1 APRAVFPSIVGRPRH 15
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100.0%; Score 80; DB 2; Length 374; 100.0%; Pred. No. 5.9e-06;

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"A multilocus gene gene genealogy concordant with host preference indicates segregation of a new species, Magnaporthe oryzae, from M. grisea.";

Mycologia 94:683-693(2002).

EMBL, ANG04735, AALS9410.1;

GO, GO:0015629, C:actin cytoskeleton; IEA.

GO, GO:0005200; F:structural constituent of cytoskeleton; IEA.
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Couch B.C., Kohn L.M.;

"A multilocus gene genealogy concordant with host preference indicates segregation of a new species, Magnaporthe oryzae, from M. grisea.";

Mycologia 94:683-693(2002).

EMBL; AX063734; AALS9409.1; -.
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Magnaporthe grisea (Rice blast fungus) (Pyricularia grisea).
Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
NCBI_TaxID=148305;
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Eukaryota; Fungi; Ascomycota; Perizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
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(TrEMBLrel. 24, Last annotation update)
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Last annotation update)
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Pred. No. 8.2e-07;
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STRAIN=ATCC 96043;
Couch B.C., Kohn L.M.;
A multilocus genealogy concordant with host preference indicates segregation of a new species, Magnaporthe oryzae, from M. grisea.";
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A multilocus gene genealogy concordant with host preference indicates segregation of a new species, Magnaporthe oryzae, from M. grisea.";
Mycologia 94:683-693(2002).
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Eukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes,
Sordariomycetes incertae sedis, Magnaporthaceae, Magnaporthe.
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GO; GO:0015629; C:actin cytoskeleton; IEA.
GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
PFam; PF00022; Actin; 1.
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SEQÜENCE 20 AA; 2141 MW; BO6CCBB097FA4ABD CRC64;
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Sordariomycetes incertae sedis, Magnaporthaceae, Magnaporthe.
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GO, GO:0015629; C:actin cytoskeleton; IEA.
GO, GO:0025200; F:structural constituent of cytoskeleton; IEA.
InterPro; IPR004000; Actin_like.
Pfam; PF00022; Actin; 1.
NON TER 20 20
SEQÜENCE 20 AA; 2141 MW; B06CCBB097FA4ABD CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Best Local Similarity 100.
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Couch B.C., Kohn L.M.;

Couch B.C., Kohn L.M.;

Auntilocus gene genealogy concordant with host preference indicates segregation of a new species, Magnaporthe oryzae, from M. grisea.";

Mycologia 94:683-693.2002).

BMBL; AR395973; AAR77895.1; -.

GO; GO:0015629; C:actin cytoskeleton; IEA.

GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.

FINEPPCO; IPRO04000; Actin_like.

Ffam; PP00022; Actin; 1.
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Eukaryota, Fungi, Ascomycota; Pezizomycotina, Sordariomycetes;
Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
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Mycologia 94:683-693(2002).

EMBL, AR395974; AR77896.1; -.
GO; GO:0015620; Cactin cytoskeleton; IEA.
GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
InterPro; IPR004000; Actin_like.
PF00022; Actin; 1.
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20 AA; 2141 MW; B06CCBB097FA4ABD CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UIN-2003 (TrEMBLrel. 24, Last annotation update)
Actin (Fragment).
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100.0%; Pred. No. 8.2e-07;
tive 0; Mismatches 0;
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Q9C2Z6;
01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2003 (TrEMBLrel. 24,
Actin (Fragment).
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Sclerotinia sclerotiorum.
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        "A multilocus gene genealogy concordant with host preference indicates segregation of a new species, Magnaporthe oryzae, from M. grisea."; Mycologia 94:683-693(2002).

EMBL; AR395972; AR77894.1; -. GO; GO:0015629; C:actin cytoskeleton; IEA.

GO; GO:0015629; C:actin cytoskeleton; IEA.

InterPro; IPR004000; Actin_like.

Pfam; PF00022; Actin; 1.
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MEDLINE=21247026; PubMed=11348503;
Carbone I., Kohn L.M.;
"A microbial population-species interface: nested cladistic and coalescent inference with multilocus data.";
Mol. Ecol. 10:947-964(2001).
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GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
InterPro; IPR004000; Actin_like.
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;
Helotiales; Sclerotiniaceae; Sclerotinia.
NCBI_TaxID=5180;
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Helotiales, Sclerotiniaceae, Sclerotinia.
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20 AA; 2141 MW; B06CCBB097FA4ABD CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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100.0%; Score 80; DB
Best Local Similarity 100.0%; Pred. No. 8.2
Matches 15; Conservative 0; Mismatches
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nes 15; Conservative
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Couch B.C., Kohn L.M.;
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                                           Carbone I., Kohn L.M.;

"A microbial population species interface: nested cladistic and coalescent inference with multilocus data.";

MOL. Ecol. 10:947-964 (2001).

EMBL; AF340963; AAK09782.1; -.

EMBL; AF340963; AAK09782.1; -.

GO; GO:0015629; C:actin cytoskeleton; IEA.

GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.

InterPro; IPR004000; Actin_like.

Pfam; PF00022; Actin, 1.

NON TER.

1 SEQÜENCE 20 AA; 2141 MW; B06CCBB097FA4ABD CRC64;
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MEDLINE=21247026; PubMed=11348503;
Carbonn I., Kohn L.M.;
"A microbial population-species interface: nested cladistic and coalescent inference with multilocus data.";
"A microbial population-species interface: nested cladistic and wol. Ecol. 10:947-964(2001).
EMBL: AF340962, AAK09781.1;
GO; GO:0015629; Cactin cytoskeleton; IEA.
GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
InterPro; IPR004000; Actin_like.
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Bukaryota, Fungi, Ascomycota, Pezizomycotina, Leotiomycetes,
Helotiales, Sclerotiniaceae, Sclerotinia.
NCBI_TaxID=5180;
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100.0%; Pred. No. 8.2e-07;
tive 0; Mismatches 0;
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STRAIN=W3-A3-2;
MEDLINE=21247026; PubMed=11348503;
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STRAIN=W2-A3-5;
MEDLINE=21247026; PubMed=11348503;
MEDLINE=21247026; PubMed=11348503;

Carbone I., Kohn L.M.;
"A microbial population-species interface: nested cladistic and coalescent inference with multilocus data.";

Mol. Ecol. 10:947-964 (2001).

EMBL; AR340958; AA409777.1;

GO; GO:0015509; F:structural constituent of cytoskeleton; IEA.

InterPro; IPR004000; Actin_like.
                                                                                                                                                                                         Carbone I., Kohn L.M.;
"A microbial population-species interface: nested cladistic and coalescent inference with multilocus data.";
Mol. Ecol. 10:447-94 (2001).
EMBL; AF340959; AAK09778.1;
EMBL; AF340959; Cactin cytoskeleton; IEA.
GO; GO:0015609; F:structural constituent of cytoskeleton; IEA.
InterPro; IPR004000; Actin_like.
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Helotiales; Sclerotiniaceae; Sclerotinia.
NCBI_TaxID=5180;
                                     Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;
Helotiales; Sclerotiniaceae; Sclerotinia.
NCBI_TaxID=5180;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Actin (Fragment)
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100.0%; Pred. No. 8.2e-07;
:ive 0; Mismatches 0;
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MEDLINE=21247026; PubMed=11348503;
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Actin (Fragment).
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                                                                                                                                     Carbone I., Kohn L.M.;
"A microbial population. species interface: nested cladistic and coalescent inference with multilocus data.";
MOI. Ecol. 10:947-964(2001).
BMBI, AR1940961, AR6094001.;
GO; GO:0015629; Caccin cytoskeleton; IEA.
GO; GO:0015629; Caccin cytoskeleton; IEA.
GO; GO:00106200; R:structural constituent of cytoskeleton; IEA.
BFG0022; Actin_like.
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GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
InterPro; IPR004000; Actin_like.
Pfam; PF00022; Actin_1.
NON_TER
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;
Helotiales; Sclerotiniaceae; Sclerotinia.
NCBI_TaxID=5180;
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Helotiales, Sclerotiniaceae, Sclerotinia.
NCBI_TaxID=5180;
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MEDLINE=21247026; PubMed=11348503;
                                                                            SEQUENCE FROM N.A.
STRAIN=W3-A1-3;
MEDLINE=21247026; PubMed=11348503;
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tive 0;
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Q9C2Z8;
01-JUN-2001 (TEMBLEE]. 17,
01-JUN-2003 (TEMBLEE]. 24,
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"A microbial population-species interface: nested cladistic and
coalescent inference with multilocus data.";
MOI. Ecol. 10:947-964(2001).
EMBL; AF340957; AAK09776.1; -.
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InterPro; IPR004000; Actin_like.
Pfam; PF00022; Actin; 1.
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GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
InterPro; IPR004000; Actin_like.
Pfam; PF00022; Actin; 1.
NON TER 1 1
SEQUENCE 20 AA; 2141 MW; B06CCBB097FA4ABD CRC64;
                                                                                                                                          Eukaryota, Fungi, Ascomycota, Pezizomycotina, Leotiomycetes,
Helotiales, Sclerotiniaceae, Sclerotinia.
NCBI_TaxID=5180;
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Bukaryota; Pungl; Ascomycota; Pezizomycotina; Leotiomycetes;
Helotiales; Sclerotiniaceae; Sclerotinia.
NCBI_TaxID=5180;
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100.0%; Score 80; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.2e-07;
Matches 15; Conservative 0; Mismatches 0; Indels
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Pred. No. 8.2e-07;
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01-UTN-2001 (TrEMBLrel. 17, Created)
01-UTN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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MEDLINE=21247026; PubMed=11348503;
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MEDLINE=21247026; PubMed=11348503;
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Best Local Similarity 100.'
Matches 15; Conservative
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4 APRAVFPSIVGRPRH 18

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

	Description	Aaw92528 Beta-acti	Abp42469 Human ova	Abb66853 Drosophil	Abp43176 Human ova		Adr38362 pigA3Cy3G	Adm05323 Human pro	ß	Aap61532 Sequence	Aar50328 Drug resi	Aab15017 Posttrans	Aay94569 Human car	Aab15016 Posttrans		Abr64271 Angiogene	0	Adb85212 Rat actin	Ade61174 Rat Prote	Adf30525 Rat angio	Adi63062 Human apo	Adi62970 Human apo	Adi63040 Human apo		Adj78489 Actin pro	Adl14103 Human sar
	ID	AAW92528	ABP42469	ABB66853	ABP43176	ABP43016	ADR38362 .	ADM05323	AAB12985	AAP61532	AAR50328	AAB15017	AAY94569	AAB15016	ABB77395	ABR64271	ABM04830	ADB85212	ADE61174	ADF30525	AD163062	AD162970	AD163040	ADL13002	ADJ78489	ADL14103
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0, 40.	ADO84/12 Human can Abm80841 Tumour-as Adn23274 Bacterial Ads88828 Amino aci	Ade88825 Amino aci Ade88826 Amino aci Ade88827 Amino aci	Aaw19799 Gamma-smo Abb58162 Drosophil Abb61322 Drosophil	Abb60354 Drosophil Abb64853 Drosophil Abb63315 Drosophil	Abr62327 Pacific w Adn03845 Antipsori Aab15014 Human car Aay94568 Human car
ADP04899 ADP12391 ADQ26098	ABO84772 ABM80841 ADN23274 ADS88828	3 ADS88825 ADS88826 ADS88827	ABB58162 ABB58162 ABB61322	ABB60354   ABB64853   ABB63315	5 ABR62327 3 ADN03845 5 AAB15014 6 AAY94568
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#### ALIGNMENTS

RESULT 1

Peptide substrate; CCT; eukaryotic type II chaperonin complex; cyclin; binding agent; substrate-binding site; SBS; substrate folding; actin; tubulin; treatment; cancer; anticancer drug; viral infection; screening; reduced toxicity. Identifying specific binding agents for substrate binding site in CCT chaperonin complex - also new peptide binding agents and their mimetics, and peptides containing a specific CCT binding site, used for treating (CANC-) INST CANCER RES ROYAL CANCER HOSPITAL. Beta-actin reference peptide substrate #2. Ź AAW92528 standard, peptide, 15 Liou AK; 98WO-GB001485. 97GB-00010762. (first entry) Hynes G, WPI; 1999-070162/06. 22-MAY-1998; 23-MAY-1997; WO9853322-A1 26-APR-1999 26-NOV-1998. Willison K, Synthetic. AAW92528; AAW92528 

Disclosure; Fig 10; 97pp; English.

This invention describes a method which uses the CCT (eukaryotic type II chaperonin) complex or part of it, for identifying a binding agent that can occupy a substrate-binding site (SBS) on the CCT complex. By binding to the CCT complex, the binding agents bloss so that biological activity of the CCT complex is affected, particularly its ability to fold substrates such as actin, tubulin and cyclin. The binding agents are useful for treatment of cancer, particularly when used in combination with an anticancer drug, or viral infections. Nucleic acid fragments are used to screen for agents, e.g. binding agents that modulate interaction between the CCT complex and a protein that is to be folded. The binding

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP43228) and to cDNAs encoding them (ABO54131-ABO56305), and also encompasses polypeptides 90% identical and polymucleotides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigen polymucleotides, antibodies against human ovarian antigens and the use of ovarian antigen polymucleotides and polypeptides in diagnosing, treating, prognosing or preventing various ovary and/or breast cancer, and metastatic tumours of ovarian or breast origin, reproductive system disorders (e.g., infertility, disorders of pregnancy, anovulation, polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndrome; PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; infection; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disorder; urinary system disorder; drug screening; gene therapy; chromosome mapping; forensic analysis; antibody preparation; cytostatic; immunomodulatory; neuroprotective;
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agents may target cells that are actively synthesising tubulin etc. (unlike known microtubule-stabilishing agents that affect all cells) should have reduced toxicity for normal cells. AAW92527-W92541 are peptide substrates used in the method of the invention
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                                                                                                                               Score 80; DB 2; I Pred. No. 5.1e-07; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antiinflammatory; gynaecological; reproductive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human ovarian antigen HOCQG94, SEQ ID NO:3601.
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                                                                                                                                                                                                                                                                                                                                      ABP42469 standard; protein; 105 AA.
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100.0%;
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Best Local Similarity 100.
Matches 15; Conservative
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wagnitis), inflammatory conditions (e.g., mastitis, cophoritis and vagnitis), immune disorders (e.g., congenital and acquired theories, autoimmune opphoritis, systemic lupus erythematosus), immune disorders (e.g., congenital and acquired theories, sutoimmune cophoritis, systemic lupus erythematosus), cespiratory disorders (e.g., anaemia), cardiovascular disorders, and uninary system disorders. Ovarian antigen polypeptides and polynucleotides may also be used in screening for compounds which modulate ovarian antigen or activity. The polynucleotides may further be used for gene therapy, chromosome mapping, in the collection of individuals and in forensic analysis, and the polypeptides may be used as food additives or to prepare antibodies useful in disease diagnosis, drug targeting and phenotyping. The present sequence represents a human ovarian antigen of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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100.0%; Pred. No. 3.9e-06;
ive 0; Mismatches 0;
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11-JUL-2000; 2000US-00614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP4328) and to CDNAs encoding them (ABQ54131-ABQ56305), and also compasses polypeptides 90% identical and polymucleotides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigen polymucleotides, antibodies against human ovarian antigens and the use of ovarian antigen polymucleotides and polypeptides in diagnosing, treating, prognosing or preventing various ovary and/or breast cancer, and metastatic tumours of ovarian or breast origin, reproductive system disorders (e.g., infertility, disorders of pregnancy, anovulation, polycystic ovary syndrome, ovarian cystes, and dysmenorrhoea), endocrine disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndrome; PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; cardiovascular disorder; respiratory disorder; neurological disorder; gene therapy; chromosome mapping; forensic analysis; antibody preparation; cytostatic; immunomodulatory; neuroprotective; antiinflammatory; gynaecological; reproductive.
                printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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ABB72072). The sequence data for this patent did not
                                                                                                         Score 80; DB 4; I
Pred. No. 5.9e-06;
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                                                                       Sequence 157 AA;
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shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and vaginitis), immune disorders (e.g., congenital and acquired immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus), blood-related disorders (e.g., anaemia), cardiovascular disorders, respiratory disorders, neurological disorders, gastrointestinal disorders of and urinary system disorders. Ovarian antigen polypeptides and polymelocides may also be used in screening for compounds which modulate ovarian antigen expression or activity. The polynucleotides may care therapy, chromosome mapping, in the identification of individuals and in forensic analysis, and the polypeptides may be used as food additives or to prepare antibodies useful in disease diagnosis, drug targeting and phenotyping. The present sequence represents a human ovarian antigen of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
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100.0%; Pred. No. 7.6e-06;
ive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                               Sequence 201 AA;
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ID ABP4
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us-09-423-351c-2.rag

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The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP4328) and to CDRAs encoding them (ABQ54131-ABQ56305), and also encompasses polypeptides 90% identical and polypucleorides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigen and the use of ovarian antigen polypucleotides and and polypeptides in diagnosing, treating, prognosing or preventing various ovary and/or breast related clsorders. Such conditions include ovarian cancer and breast cancer, and disorders (e.g., infertility, disorders origin, reproductive system clsorders (e.g., infertility, disorders origin, reproductive system disorders (e.g., infertility, disorders origin, reproductive system closystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine disorders, infertions (e.g., chlamydia, HIV, toxoplasmosis, and toxic shock syndrome), inflammatory conditions (e.g., mastitis, cophoritis and immunodeficiencies, autoimmune ophoritis, systemic alsorders, autoimmune ophoritis, systemic alsorders, crepirated disorders (e.g., anamia), cardiovascular disorders and urinary system disorders. Devaian antigen polypeptides and completed disorders (e.g., anamia), cardiovascular antibodies (e.g., anamia), and the polypeptides may be used in forensic analysis, and the sequence data for this patent did not form part of the printed sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ftp.wipo.int/pub/published_pct_sequences
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Gaps ; 0 Length 204; 0; Indels 100.0%; Score 80; DB 5; L 100.0%; Pred. No. 7.8e-06; Mismatches ; 0 Query Match 100. Best Local Similarity 100. Matches 15; Conservative Sequence 204 AA;

15 65 51 FPSIVGRPRHOGVMV 1 FPSIVGRPRHQGVMV g ð

ADR38362 standard; protein; 310 AA. 18-NOV-2004 ADR38362; ADR38362 

(first entry)

pigA3Cy3GFP plasmid protein product (Cycle3 GFP under an actin promoter).

piggyBac; transposon; transposase; gene transfer; plasmid; Cycle3 GFP; actin promoter.

Bombyx mori

Synthetic. Unidentified.

/note= "Encoded by GCC" Location/Qualifiers Misc-difference 20

JP2004236642-A

26-AUG-2004.

10-FEB-2003; 2003JP-00032306.

10-FEB-2003; 2003JP-00032306.

(TORA ) TORAY IND INC

WPI; 2004-608233/59.

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N-PSDB; ADR38361
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Introducing foreign gene into insect cell, involves introducing DNA having foreign gene integrated between inverted repeat sequences of piggyBac transposon and piggyBac transposase that acts on inverted repeat sednence.

Disclosure; Page; 25pp; Japanese.

This invention relates to a novel method for introducing a foreign gene into an insect cell. Specifically, it refers to a foreign gene occurring between inverted repeat sequences of a piggyBac transposon and using a piggyBac transposon and using a piggyBac transposon and using a piggyBac transposonse for gene transfer to give a high recombinant efficiency. The present invention describes the insect cell as that of Lepidoptera insect origin, preferably it is the silk worm Bombyx mori, and stable integration occurs into the genome of this insect using the transposase enzyme. In particular, this gene transfer method uses the plasmid pigA3Cy3GFP which contains a Cycle3 GFP gene expressed under a silk worm actin promoter. As promoter, between a pair of inverted repeat equences of the transposon pigGyBac. This polypeptide sequence is the protein product from the pigA3Cy3GFP plasmid DNA that represents the silkworm actin promoter controlling expression of the Cycle3 GFP gene silkworm are membedded protein in the sequence is the given in an exemplification of the invention. NOTE: This sequence is cluther within the specification.

Sequence 310 AA;

Gaps ô 100.0%; Score 80; DB 8; Length 310; 100.0%; Pred. No. 1.2e-05; ive 0; Mismatches 0; Indels 100.0%; Pic Query Match Best Local Similarity 100.0 Matches 15; Conservative

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1 FPSIVGRPRHQGVMV 15

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46 32 FPSIVGRPRHQGVMV

RESULT 7 ADM05323

ADM05323 standard; protein; 342 AA. 20-MAY-2004 (first entry) ADM05323;

Human protein of the invention SEQ ID NO:4008. 

human; gene therapy; diagnostic marker; pharmaceutical.

Homo sapiens.

EP1347046-A1

24-SEP-2003.

12-APR-2002; 2002EP-00008400.

22-MAR-2002; 2002JP-00137785.

(REAS-) RES ASSOC BIOTECHNOLOGY.

Tamechika I; Otsuki T, Wakamatsu A, Sato H, Ishii S; Hio Y, Otsuka K, Nagai K, Irie R, Tamecl Otsuka M, Nagahari K, Masuho Y; Isogai T, Sugiyama T, Yamamoto J, Isono Y, Seki N, Yoshikawa T,

WPI; 2003-723558/69. N-PSDB; ADM02880.

New polynucleotides and polypeptides are useful in gene therapy, for developing a diagnostic marker or medicines for regulating their expression and activity, or as a target of gene therapy.

Claim 1; SEQ ID NO 4008; 305pp; English.

us-09-423-351c-2:rag

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention provides a treatment for sickle cell anaemia, which comprises administering a reducing agent. The treatment inhibits the formation of irreversible sickled cells (ISC) and reverses ISC formation in the blood. The present sequence represents the human beta-actin protein. The sequence is used in the invention to demonstrate that a distulphide bridge is formed between cysterines 284 and 373 in ISC beta-actin as a post-translational modification. The reducing agent used in the treatment acts to correct this post-translational modification
                           polypeptide. A polynucleotide of the invention may have a use in gene therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful as a primar for synthesizing the polynucleotide or as a probe for detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are useful in gene therapy, for developing a diagnostic marker or medicines for regulating their expression and activity, or as a target of gene therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides are useful as pharmaceutical agents. The present sequence represents a protein sequence of the invention.
                  The invention relates to a novel human polynucleotide and the encoded
                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Beta actin; post translational modification; sickle cell anaemia; irreversibly sickled cell; ISC; treatment.
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                                                                                                                                                                                                                                          Score 80; DB 7; Length 342; Pred. No. 1.3e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB12985 standard; protein; 374 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human beta-actin protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 17; Fig 5B; 53pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                        Query Match 100.
Best Local Similarity 100.
Matches 15; Conservative
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                                                                                                                                                                                                           Sequence 342 AA;
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Beta-actin gene and regulatory elements - used for expression of polypeptide(s) in mammalian host cells.

(STRD ), UNIV LELAND STANFORD JUNIOR.

85EP-00111225.

05-SEP-1985;

19-MAR-1986. EP174608-A.

Gunning PW;

Leavitt JC, Kedes LH, WPI; 1986-077015/12. N-PSDB; AAN60172.

Actin fibre; actin film; recombinant beta-actin.

Homo sapiens

AAP61532 standard; protein; 375 AA

AAP61532

(revised)
(first entry)

25-MAR-2003 13-SEP-1991

AAP61532;

Sequence of beta-actin

30 FPSIVGRPRHOGVMV 44

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             structural gene; expression vector; selective; marker; thymidine-kinase deleted cell.
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                                                                                                                                                                                                                                                                                                Example; Page 23-24; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR50328 standard; protein; 375 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drug resistant structural protein.
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Gaps

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Indels

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Mismatches

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100.0%; 100.0%;

Query Match 100. Best Local Similarity 100. Matches 15; Conservative

Score 80; DB 3; Length 374; Pred. No. 1.5e-05;

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The present invention relates to human cardiac actin (ACTC). Genotypic analyses show that ACTC is linked to idiopathic dilated cardiomyopathy (IDC). The ACTC gene maps to chromosome 15q14. Six PCR primer pairs (AAA49020 to AAA49031) have been developed to allow analysis of the six exons of ACTC. Studies of two families with IDC showed the presence of two mutations, one in exon 5 and one in exon 6. The present sequence is a mutant of posttranslationaly modified ACTC without the initial two residues. The mutation is a clu to Gly mutation at position 361. The ACTC protein may be used in a variety of methods for drug screening and for rational drug design. The ACTC gene may be used to treat IDC by gene therapy. Analysis of the ACTC gene may be used to treat IDC by gene therapy. Analysis of the ACTC gene provides early identification of subjects likely to develop or who already have IDC. Note: The present sequence is not shown in the specification but is derived from the ACTC sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is human cardiac actin (ACTC) protein, without the initial Met-Cys which is posttranslationally removed. Genotypic analyses show that ACTC is linked to idiopathic dilated cardiomyopathy (IDC). The ACTC gene maps to chromosome 15q14. Six PCR primer pairs (AAA49020 to AAA49031) have been developed to allow analysis of the six exons of ACTC. Studies of two families with IDC showed the presence of two mutations,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New cardiac actin gene comprising histidine to arginine or glycine glutamic acid substitution, useful in the diagnosis of diseases associated with the mutation, specifically idiopathic dilated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human cardiac actin protein after posttranslational modification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 80; DB 3; Length 375; 100.0%; Pred. No. 1.5e-05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cardiac actin; ACTC; human; gene therapy; IDC; 15q14; idiopathic dilated cardiomyopathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY94569 standard; protein; 375 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-00106217.
                                          Claim 3; Page; 36pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-375488/32.
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                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 375 AA;
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cardiomyopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-JUN-1998;
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                                                                                                                                                                                                                                              Expression vector contg. drug resistant marker gene - useful for transformation of thymidine kinase-deleted human cells for high levels of
                                                                                                                                                                                                                                                                                                                                                                          This sequence is encoded by a drug resistant structural gene which may be used in the expression vector of the invention. This gene is used as the selective marker in the vector. The resulting vector may be used to transform a thymidine-kinase deleted cell allowing introduction of a foreign structural gene. The transformed cell may be used to produce large amounts of useful protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New cardiac actin gene comprising histidine to arginine or glycine to glutamic acid substitution, useful in the diagnosis of diseases associated with the mutation, specifically idiopathic dilated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Posttranslationaly modified human cardiac actin mutant E361G.
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                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 5-7; 7pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB15017 standard; protein; 375 AA.
                                          92JP-00045939.
                                                                                      92JP-00045939.
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                                                                                                                                                                                                                                                                                           foreign protein prodn.
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N-PSDB; AAA73739.
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Best Local Similarity
                                                                                                                                                                             1994-094836/12.
                                                                                                                                (TOYM ) TOYOBO KK.
                                                                                                                                                                                                  N-PSDB; AAQ44861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 375 AA;
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                                                                                    31-JAN-1992;
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                                          31-JAN-1992;
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15-FEB-1994
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Matches

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RESULT 11

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sequence described in AAY94569
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to human cardiac actin (ACTC). Genotypic analyses show that ACTC is linked to idiopathic dilated cardiomyopathy (IDC). The ACTC gene maps to chromosome 15q14. Six PCR primer pairs to AAA49020 to AAA49031) have been developed to allow analysis of the six exons of ACTC. Studies of two families with IDC showed the presence of two mutations, one in exon 5 and one in exon 6. The present sequence is a mutant of posttranslationaly modified ACTC without the initial two protein may be used in a variety of methods for drug screening and for rational drug design. The ACTC gene may be used to treat IDC by gene therapy. Analysis of the ACTC gene provides early identification of subjects likely to develop or who already have IDC. Note: The present sequence is not shown in the specification but is derived from the ACTC
one in exon 5 and one in exon 6. The mutations are G to A in codon 312 (Arg312His) and A to G in codon 361 (Glu361Gly). The ACTC protein may be used in a variety of methods for drug screening and for rational drug design. The ACTC gene may be used to treat IDC by gene therapy. Analysis of the ACTC gene provides early identification of subjects likely to develop or who already have IDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S
                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New cardiac actin gene comprising histidine to arginine or glycine glutamic acid substitution, useful in the diagnosis of diseases associated with the mutation, specifically idiopathic dilated
                                                                                                                                                                                                                                                                                                                                               Cardiac actin; ACTC; human, gene therapy; IDC; chromosome 15q14; idiopathic dilated cardiomyopathy; mutant; mutein.
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                                                                                                                                                                                                                                                                                                                          Posttranslationaly modified human cardiac actin mutant R312H.
                                                                                                              Length 375;
                                                                                                 Score 80; DB 3; Length 3. Pred. No. 1.5e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Wild-type Arg substituted by His"
                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                 AAB15016 standard; protein; 375 AA.
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                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                      Conservative
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                                                                                               Query Match
Best Local Similarity
Local 15; Conserve
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N-PSDB; AAA73738.
                                                                                      Sequence 375 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                     sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to in vitro methods for the detection of skin stress and/or skin ageing in humans and animals based on the determination of spondin 2, cathepsin L, actin gamma 1 or vimentin fragments secreted by fibroblast from the skin under test. Use of the methods in a test for potential cosmetics and pharmaceuticals with an effect on these skin conditions and products contexining vimentin fragments are also included. Products contexining vimentin fragments are effective in the regulation, especially maintenance, of skin homeostasis
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                                                                                       Gaps
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actin gamma 1; vimentin; fibroblast; skin; cosmetic; pharmaceutical.
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                                          Length 375;
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                                        Score 80; DB 3; L
Pred. No. 1.5e-05;
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Pred. No. 1.5e-05;
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                                                                                                                                                             31 FPSIVGRPRHQGVMV
                                                                                       15; Conservative
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les 15; Conser
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Sequence 375 AA;
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                                          Query Match
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The invention relates to the isolation of novel genes (ACF3446-ACF34559)

cencoding proteins (ABR64180-ABR64281) involved in the process of
angiogenesis. The nucleic acid molecules are useful in identifying and/or
obtaining full-length human genes involved in an angiogenic process. The
cobtaining full-length human animals derived from these are useful for
concleic acid molecule, polypeptides or complexes encoded, cells or
concleic acid molecule, polypeptides or complexes encoded, cells or
concleic acid molecule, polypeptides or complexes encoded, cells or
concleic acid molecule, planman animals derived from these are useful
concleic acid molecule, planman animals derived from treating
angiogenesis-related disorders. They are also useful for diagnosing,
involves uncontrolled or enhanced angiogenesis or is a disorder in which
a decreased vasculature is of benefit (e.g. cancer, rheumatoid arthritis,
concleic acid sections or involves inappropriately arrested or decreased
angiogenesis or is a disorder in which an expanding vasculature is of
congiseration or involves inappropriately arrested or decreased
angiogenesis or is a disorder in which an expanding vasculature is of
modulator of expression or activity of the polypeptide encoded by the
concleic acid sequence is useful for manufacturing a medicament for the
concert the provest of the polypeptide corresponds
                                                                                                            antirheumatic; antiarthritic; antidiabetic; ophthalmological;
                                                                                                                              antipsoriatic; antiarteriosclerotic; cardiant; vasotropic; angiogenesis; gene therapy; vasculature; cancer; rheumatoid arthritis; psoriasis; diabetic retinopathy; cardiovascular disease; atherosclerosis; ischemic limb disease; coronary artery disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          prognosticating or treating an angiogenesis-related disorder, e.g. cancer, rheumatoid arthritis, diabetic retinopathy, psoriasis or cardiovascular diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New angiogenic genes and polypeptides, useful for diagnosing,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 15; SEQ ID NO 206; 90pp; English.
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11-OCT-2001; 2001AU-00008210.
29-OCT-2001; 2001AU-00008532.
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                                                               Angiogenesis protein BNO369
                    15-OCT-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BION-) BIONOMICS LTD.
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                                                                                                          Cytostatic;
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Gaps
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    Length 375;
                         0; Indels
  Score 80; DB 6; I
Pred. No. 1.5e-05;
; Mismatches 0;
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   100.08;
Query Match
Best Local Similarity 100.(
Matches 15; Conservative
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ઠે 셤 Search completed: April 8, 2005, 10:50:42 Job time : 64.4 secs

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INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
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2, Appli
6100, Ap
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33, Appl
53, Appl
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                                                                      8, 2005, 09:58:57; Search time 17.5333 Seconds (without alignments) 63.863 Million cell updates/sec
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6ZOWB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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-09-621-976-6521
-08-505-250-17
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US-09-949-016-6656
US-09-949-016-8452
US-09-949-016-7725
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US-09-949-016-9424
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US-09-919-172-33
US-09-917-254-53
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US-09-306-446C-2
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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#### ALIGNMENTS

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RESULT
US-08-609-236-6
Sequence 6, Application US/08609216
Patent No. 6087398
SEQUENCER: Republication US/08609216
SEQUENCER: SEQUENCES: 6 608739861 Sickle Cell Anemia Treatment UNDER OF SEQUENCES: 6 608739861 Sickle Cell Anemia Treatment TITLE OF SEQUENCES: 6 608739861 Sickle Cell Anemia Treatment UNDER OF SEQUENCES: 6 608739861 Sickle Cell Anemia Treatment TITLE OF SEQUENCES: 6 608739861 SICKLES OF SEQUENCES: 6 608739861 STREET: 8011 Candle Lane
CONFIDENT READALE FORM: Macintosh Maci
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APPLICANT: Olson, Timothy M.
TITLE OF INVENTION: Actin Mutations in Dilated
TITLE OF INVENTION: Cardiomyopathy, a Heritable Form of Heart Failure
CORRESPONDENCE: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                              Gaps
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Fatent No. 5840528
GENERAL INPORMATION:
FAPLICANT: Van Ooyen, Albert Johannes Joseph
TITLE OF INVENTION: Transformation of Phaffia rhodozyma
NUMBER OF SEQUENCES: 14
CORRESPONDENCE MADRESS:
ADDRESSERE: Mortison & Poerster
STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
CITY: Washington, D.C.
COUNTX: USA
CONPUTER: Lab PC Compatible
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BADABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: Patentin Release #1.0, Version #1.25
CURRING SYSTEM: DATA:
PLING DATE: USAOR4151
FILING DATE: USAOR4151
FILING DATE: USAOR4151
FILING DATE: USAOR41151
FILING DATE: USAOR41151
FILING DATE: USAOR41151
                                                                                                  Score 80; DB 3; Length 374; Pred. No. 6.9e-06;
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; Sequence 16, Application US/09106217
; Patent No. 6063576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: MUTABLIGE, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2461
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELER: 90-4030
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acids
TYPE: amino acid
                                                                                                Query Match
Best Local Similarity 100.0%; Pr
Matches 15; Conservative 0;
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Best Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-494-151-14`
                                                          US-08-609-236-6
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APPLICANT: Furness, Michael
APPLICANT: Furness, Michael
APPLICANT: Buchbinder, Jenny
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
FILE REPRENCE: PA-0041 US
CURRENT PALICATION NUMBER: US/09/976,594
CURRENT FILING DATE: 2001-10-12
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 1143
SOFTWARE: PERL PROGRAM
SEQ ID NO 731
LENGTH: 375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
STREET: 555 Thirteenth Street, N.W., Suite 701 East
STREET: Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 80; DB 3; I
Pred. No. 6.9e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/106,217
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-976-594-731
; Sequence 731, Application US/09976594
Patent No. 6673549
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Saxe, Stephen A.
REGISTRATION NUMBER: 38,609
REFRENCE/DOCKET NUMBER: 2323
TELEPCOMMUNICATION INFORMATION:
TELEPHONE: 202-783-6040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 202-783-6031
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31 FPSIVGRPRHQGVMV 45
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Best Local Similarity 100.
Matches 15; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Teches 15; Conservat
                                                                 Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                      U.S.A.
                                                                                    STATE: DC
COUNTRY: U.
ZIP: 20004
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Gaps

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APPLICANT: Keating, Mark T.
APPLICANT: Olson, Timethy M.
ITLE OF INVENTION: Actin Mutations in Dilated
TITLE OF INVENTION: Cardiomyopathy, a Heritable Form of Heart Failure
NUMBER OF SEQUENCES: 18
ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
                                            Length 376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 80; DB 3; Length 377; 100.0%; Pred. No. 7e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
STREET: 555 Thirteenth Street, N.W., Suite 701 East
STREET: Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.30
CURRANT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/106,217
                     100.0%; Score 80; DB 4; Lo
100.0%; Pred. No. 6.9e-06;
Nicomatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                    US-09-106-217-2; Sequence 2, Application US/09106217; Sequence 2, Application US/09106217; Patent No. 6063576; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/ACENT INFORMATION:
NAME: Saxe, Stephen A.
REGISTRATION NUMBER: 38,609
REFRENCE/DOCKET NUMBER: 2323
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-783-6040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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Best Local Similarity 100.0%;
Matches 15; Conservative C
                                                                                                                                                                               32 FPSIVGRPRHQGVMV 46
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                                                                                         Conservative
                                                                                                                              1 FPSIVGRPRHQGVMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 202-783-6031
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , MOLECULE TYPE: protein US-09-106-217-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Washington STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
                                Query Match
Best Local Similarity
Matches 15; Conser
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US-09-949-016-6100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U
ZIP: 20004
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Fatent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: 00/241,755

PRIOR PELING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOUTHWARE: PERSENG FOR WINDOWS VERSION 4.0
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                                                   GENERAL INFORMATION:
APPLICANT: McHugh, Kirk M.
TITLE OF INVENTION: DIAGNOSTIC TEST FOR DETERMINING
TITLE OF INVENTION: MALIGNANCY OF SMOOTH MUSCLE TUMORS
INTHER OF SEQUENCES: 4
CORRESPONDENCE ADDRESSE: Woodcock Washburn Kurtz Mackiewicz &
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
ADDRESSEE: Woodcock Washburn Kurtz Packiewicz &
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                         COUNTRY: US.

ZIP: 19103
ZUP: 19103
ZUPTUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
PLING DATE:
CLASSIPICATION WUMBER: US/08/588,113
FLING DATE:
CLASSIPICATION WUMBER: US/08/588,113
REFERENCE/DOCKET NUMBER: 35,152
REFERENCE/DOCKET NUMBER: 35,152
REFERENCE/DOCKET NUMBER: 35,152
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3439
TELEPHONE: 215-568-3439
TELEPHONE: 215-568-3439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 80; DB 1; I 100.0%; Pred. No. 6.9e-06; iive 0; Mismatches 0;
                                       Sequence 2, Application US/08588113 Patent No. 5710003
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Best Local Similarity 100...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
TOPOLOGY: linear
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LENGTH: 376
TYPE: PRT
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-949-016-6100
                       US-08-588-113-2
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                                                                                                                                                       1 FPSIVGRPRHQGVMV 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Human
US-09-949-016-10757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Human
US-09-949-016-9424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 12
US-09-949-016-10757
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7721
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APPLICAMT: VENTER, J. Craig et al.

APPLICAMT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR PILING DATE: 2000-10-20

PRIOR PELING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: REALESEQ FOR WINDOWS Version 4.0

SEQ ID NO 7721
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US-09-917-254-53
i Sequence 53. Application US/09917254
j Petent NO. 6703204
j GENERAL INFORMATION:
j APPLICANT: Matter, George
j APPLICANT: Baak, Jan
TITLE OF INVENTION: Prognostic Classification of Breast Cancer
j TITLE OF INVENTION: Prognostic Classification of Breast Cancer
j TITLE OF INVENTION: Prognostic Classification of Breast CURRENT PILING DATE: 2001-07-27
j FRICR FILING DATE: 2001-07-28
j NUMBER OF SEQ ID NOS: 102
j SOFTWARE: PatentIn version 3.0
j SEQ ID NO 53
LENGTH: 377
j TYPE: PRT
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Best Local Similarity 100.0%; Pred. No. 7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                             Length 377;
                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                             FEATURE:

NAME/KEY: misc_feature

OTHER INFORMATION: Incyte ID No. 6673545 1709118CD1

US-09-919-172-33
                                                                                                                                                                                                                                                           100.0%; Score 80; DB 4;
100.0%; Pred. No. 7e-06;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7721, Application US/09949016
Patent No. 6812339
  PRIOR APPLICATION NUMBER: 60/222,469
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 102
SOFTWARE: PERL Program
SEQ ID NO 33
LENGTH: 377
                                                                                                                                                                                                                                                                                                                                        1 FPSIVGRPRHQGVMV 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33 FPSIVGRPRHOGVMV 47
                                                                                                                                                                                                                                                             Query Match 100.
Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo Sapiens
US-09-917-254-53
                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-949-016-7721
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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REPERENCE: CL001307
CURRENT APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-10-03
PRIOR PLICE DATE: 2000-10-03
PRIOR PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PLICE DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 2007012
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                              US-09-949-016-9424

j Sequence 9424, Application US/09949016
j Patent No. 6812339
general No. 6812339
general No. 6812339
j Taten No. 6812339
j TITLE OF INVENTION: DOLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
j FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: 60/241,755
prior APPLICATION NUMBER: 60/241,755
prior APPLICATION NUMBER: 60/241,755
prior APPLICATION NUMBER: 60/237,768
prior PILING DATE: 2000-10-03
prior FILING DATE: 2000-0-03
prior PILING DATE: 2000-09-08
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Pred. No. 7.4e-06;
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    Score 80; DB 4; Length 386;
Pred. No. 7.1e-06;
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Query Match
100.0%; Score 80; DB
Best Local Similarity 100.0%; Pred. No. 7.1
Matches 15; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
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Sequence 6521, Application US/09621976

Patent No. 6639063

GRUERAL INFORMATION:
APPLICANT: Jobert, S.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET. 054PR2

CURRENT APPLICATION NUMBER: US/09/621,976

CURRENT FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 19335

SOFTWARE: Patent.pm

SEQ ID NO 6521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 75; DB 4; I
Pred. No. 8.4e-06;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Xaa = Leu, Val
US-09-621-976-6521
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Best Local Similarity 93.3%;
Matches 14; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 62
OTHER INFORMATION: Xaa
NAME/KEY: UNSURE
                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: UNSURE
                                     US-09-621-976-6521
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APPLICANT: Keith Weinstock et al
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT PAPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR PILING DATE: 1998-02-13
PRIOR PILING DATE: 1998-08-13
PRIOR FILING DATE: 1998-08-13
                                                                                                                                                                                   RESULT 13

US-09-940-016-11313

Sequence 11313, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

PILE REFERENCE: CL001307

CURRENT FILING DATE: 2000-04-14

PRIOR PLILNG DATE: 2000-10-20

PRIOR PLILNG DATE: 2000-10-20

PRIOR PLILNG DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03
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Pred. No. 7.5e-06;
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Pred. No. 2.3e-05;
2; Mismatches 0; Indels
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                                     Indels
           Pred. No. 7.5e-06; Mismatches 0;
100.0%; Pred. ...
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Best Local Similarity 100.0%; Pred. No. 7.5
Matches 15; Conservative 0; Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity 86.7%;
Matches 13; Conservative
                                                                                                        58 FPSIVGRPRHQGVMV 72
                                                                               1 FPSIVGRPRHQGVMV 15
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                                  15; Conservative
             Best Local Similarity
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LENGTH: 404
                                Matches
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/cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
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/cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
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/cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 3601, Ap	Sequence 184471,	Sequence 4308, Ap	Sequence 4148, Ap	Sequence 56, Appl	Sequence 4008, Ap	Sequence 68, Appl	Sequence 93, Appl	Sequence 88, Appl	Sequence 5927, Ap	Sequence 94, Appl	Sequence 82, Appl	Sequence 101, App
SUMMARIES	aı	US-10-264-049-3601	US-10-424-599-184471	US-10-264-049-4308	US-10-264-049-4148	US-10-002-631C-56	US-10-108-260A-4008	US-10-322-281-68	US-10-205-194-93	US-10-316-253-88	US-10-369-493-5927	US-10-205-331-94	US-10-260-708-82	US-10-341-434-101
	DB	15	15	15			15				15			15
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	% Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
	Score	80	80	80	80	80	80	80	80	80	80	80	80	80
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Sequence 33, Appl Sequence 64, Appl Sequence 4, Appli Sequence 63, Appl Sequence 1436, Ap	14,44,44	28290 42770 28333 2436, 17991	2024 4567 4609 1620 2228 2238	283336, 66124, 121952, 148877, 198295,	Sequence 47239, A Sequence 36824, A Sequence 42317, A Sequence 52458, A
US-09-91 US-10-2 US-10-3 US-10-3 US-10-3	US-10-477-369-1 US-10-029-386-320 US-10-767-701-473 US-10-424-599-280 US-10-424-599-280	US-10-424-599 US-10-767-701 US-10-424-599 US-10-369-493 US-10-437-963	US-10-437-963 US-10-767-701 US-10-36-701 US-10-334-599 US-10-424-599 US-10-424-599	US-10-424-599-2833 US-10-425-114-6612 US-10-437-963-1488 US-10-437-963-1488 US-10-437-963-1982	. US-10-767-701-47239 . US-10-425-114-36824 . US-10-425-114-42317 . US-10-425-114-52458
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#### ALIGNMENTS

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NAME/KEY: MISC_PEATURE

1 LOCATION: (103)

2 OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids

US-10-264-049-3601
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Sequence 3601, Application US/10264049
; Sequence 3601, Application US/10264049
; Publication No. US2004000557941
; GENERAL INPORMATION:
; APPLICANT: Birse et al.;
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA13791
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PALENTIN Ver. 3.1
; SEQ ID NO 3601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 80; DB 15;
100.0%; Pred. No. 2e-05;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
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32 FPSIVGRPRHQGVMV 46

1 FPSIVGRPRHQGVMV 15

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RESULT 2

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) OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids US-10-264-049-4308
LOCATION: (145)
OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (174)
OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
                                                                                                              equals any of the twenty naturally occurring L-amino acids
                                                                                                                                                                                                      equals any of the twenty naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 201;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Birse et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PAI33P1
CURRENT APPLICATION NUMBER: US/10/264,049
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: PCT/US01/18569
PRIOR FILING DATE: 2000-00-07
PRIOR FILING DATE: 2000-00-07
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Publication No. US20030157486A1
GENERAL INFORMATION:
APPLICANT: Graff, Jonathon M.
TITLE OP INVENTION: METHODS TO IDENTIFY SIGNAL SEQUENCES
FILE REFERENCE: A34943 090495.0243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 80; DB 15; 100.0%; Pred. No. 3.9e-05;
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100.0%; Pred. No. 3.9e-05;
ive 0; Mismatches 0;
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; Sequence 4148, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
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SOFTWARE: Patentin Ver. 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.
Best Local Similarity 100.
Matches 15; Conservative
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CRGANISM: Homo sapiens
US-10-264-049-4148
                                                                                                                OTHER INFORMATION: Xaa
                                                                                                                                                                                                              OTHER INFORMATION: Xaa
                                                                                                                                                                                                                                                       NAME/KEY: MISC FEATURE LOCATION: (172)
                                                                                                                                                                                                                                                                                                                                                NAME/KEY: MISC FEATURE LOCATION: (174)
                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (180)
                                                                    NAME/KEY: MISC FEATURE
                                                                                                                                                               NAME/KEY: MISC FEATURE LOCATION: (159)
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Best Local Similarity
Matches 15; Conserv
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LENGTH: 204
                                                                                               LOCATION:
                                                                                                                                                                                                                                      FEATURE:
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                                                      GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Caro Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (5323) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 184471
LENGTH: 142
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA1391
CURRENT APPLICATION NUMBER: US/10/264,049
CURRENT FILING DATE: 2002-10-04
PRIOR PILING DATE: 2001-06-07
PRIOR FILING DATE: 2001-06-07
PRIOR FILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 4360
SOFTWARE: Patentin Ver. 3.1
LENGTH: 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 80; DB 15; Length 142;
Pred. No. 2.7e-05;
Mismatches 0; Indels
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US-10-424-599-184471
                        Sequence 184471, Application US/10424599
Publication No. US20040031072A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4308, Application US/10264049 Publication No. US20040005579A1 GENERAL INFORMATION:
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100.0%; Pre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40 FPSIVGRPRHQGVMV 54
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Best Local Similarity 100.0
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: MISC FEATURE LOCATION: (135)
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NAME/KEY: MISC_FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Glycine max
       US-10-424-599-184471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-264-049-4308
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US-10-205-194-93
. Sequence 93, Application US/10205194
; Publication No. US20030134301A1
; GENERAL INFORMATION:
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31 FPSIVGRPRHQGVMV 45
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CRGANISM: Rattus norvegicus
US-10-316-253-88
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Best Local Similarity 100.
Matches 15; Conservative
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Best Local Similarity
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; Sequence 68, Application US/10322281
; Publication No. US20040126762A1
; Fublication No. US20040126762A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc S. Malandro
; TITLE OF INVENTION: NOVel Compositions and Methods in Cancer; TITLE OF INVENTION: NOVel Compositions and Methods in Cancer; CURRENT APPLICATION NUMBER: US/10/322,281
; CURRENT FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 68
; LENGTH: 371
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100.0%; Score 80; DB 16; Length 371;
Best Local Similarity 100.0%; Pred. No. 7.2e-05;
Matches 15; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4000, Application US/10108260A; bublication No. US20040005560A1; publication No. US20040005560A1; GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: No. US20040005560A1e1 full length cDNA FILE REFERENCE: H1-A0106; CURRENT APPLICATION NUMBER: US/10/108,260A; CURRENT FILING DATE: 2002-03-27; NUMBER OF SEQ ID NOS: 5458; SOFTWARE: Patentin Ver. 2.1; SEQ ID NO 4008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0%; Score 80; DB 15; Length 342;
Best Local Similarity 100.0%; Pred. No. 6.6e-05;
Matches 15; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                     100.0%; Score 80; DB 14; Length 219; 100.0%; Pred. No. 4.2e-05; tive 0; Mismatches 0; Indels
  CURRENT APPLICATION NUMBER: US/10/002,631C
                       CURRENT FILING DATE: 2001-10-31
PRIOR APPLICATION NUMBER: 60/309
PRIOR FILING DATE: 2001-06-21
NUMBER OF SEQ ID NOS: 324
SOFTWARE: FASEUSEQ for Windows Version 4.0
SEQ ID NO 56
LENGTH: 219
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Best Local Similarity 100.05
Matches 15; Conservative
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; ORGANISM: Homo sapiens
US-10-322-281-68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
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US-10-002-631C-56
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APPLICANT: Barner-Lambert Company
APPLICANT: Lee, Kevin
APPLICANT: Discon, Alietair
APPLICANT: Discon, Alietair
APPLICANT: Discon, Alietair
APPLICANT: Discon, Alietair
APPLICANT: Pinnock, Robert
APPLICANT: Pinnock, Robert
TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
FILE REFERENCE: WL-A-018201
CURRENT APPLICATION NUMBER: US/10/205,194
CURRENT FILING DATE: 2200-07-24
PRIOR PAPLICATION NUMBER: GB 0118354.0
PRIOR FILING DATE: 2001-07-27
NUMBER OF SEQ ID NOS: 177
SOFTWARE Patentin Ver. 2.1
SEQ ID NO 93
LENGTH: 375
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Sequence 88, Application US/10316253

Publication No. US20030162706A1

GENERAL INFORMATION:
APPLICANT: The Procter & Gamble Company
APPLICANT: Peters, Kevin
APPLICANT: Wang, Feng
APPLICANT: Wang, Feng
APPLICANT: Wang, Feng
APPLICANT: Wang, Rength
TITLE OF INVENTION: Angiogenesis Modulating Proteins
FILE REFERENCE: 8865M
CURRENT FILING DATE: 2002-12-10
PRIOR APPLICATION NUMBER: US 60/355,295
PRIOR APPLICATION NUMBER: US 60/355,295
PRIOR PILING DATE: 2002-02-08
NUMBER OF SEQ ID NOS: 308
SOFTWARE: PatentIn version 3.1
SEG ID NO 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Cytoplasmic gamma isoform of actin US-10-205-194-93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 80; DB 14;
100.0%; Pred. No. 7.2e-05;
tive 0; Mismatches 0;
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US-10-369-493-5927
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Gaps
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Sequence 101, Application US/10341434

Publication No. US20030215835A1

PUBLICATION:
TITLE OF INVENTION:
PLIE REPERENCE: 9U 204 205 NI

CURRENT APPLICATION NUMBER: US/10/341,434

CURRENT PILING DATE: 2003-07-18

PRIOR PRILING DATE: 2002-01-15

PRIOR PILING DATE: 2002-01-15

PRIOR PILING DATE: 2002-01-15

NUMBER: OF SEQ ID NOS: 238

SOFTWARE: Patentin version 3.1

SEQ ID NO 101
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  APPLICANT: Old, Lloyd
TITLE OF INVENTION: Human Sarcoma-Associated Antigens
FILE REFERENCE: L00464/10138
CURRENT APPLICATION NUMBER: US/10/260,708
CURRENT FILING DATE: 2002-09-30
NUMBER OF SEQ ID NOS: 96
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 80; DB 15; Best Local Similarity 100.0%; Pred. No. 7.2e-05; Matches 15; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 14
US-09-019-172-33
i Sequence 33, Application US/09919172
j Patent No. US20020119463A1
j GENERAL INPORMATION:
APPLICANT: Turner, Christopher M.
TITLE OF INVENTION: PROSTATE CANCER MARKERS
FILE REPERENCE: PA.0036 US
CURRENT APPLICATION NUMBER: US/09/919,172
CURRENT APPLICATION NUMBER: 05/222,469
PRIOR RILING DATE: 2001-07-38
j NUMBER OF SEQ ID NOS: 102
s SOFTWARE: PERL PROGRAM
s SEQ ID NO 33
j LENGTH: 377
TURNER OF SEQ ID NOS: 102
s SOFTWARE: PERL PROGRAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: homo sapiens
US-10-260-708-82
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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Best Local Similarity
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                                                                                                                                                                                                    SEQ ID NO 82
LENGTH: 375
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100.0%; Pred. No. 7.2e-05;
tive 0; Mismatches 0;
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Pred. No. 7.2e-05;
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Best Local Similarity 100.0%; Pred. No. 7.2
Matches 15; Conservative 0; Mismatches
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Cytoplasmic beta-actin US-10-205-331-94
Sequence 5927, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 82, Application US/10260708; Publication No. US20040063101A1; GENERAL INFORMATION: APPLICANT: Scanlan, Matthew APPLICANT: Lee, Sang-Yull
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-5927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31 FPSIVGRPRHQGVMV 45
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ORGANISM: Rattus norvegicus
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Best Local Similarity 100.0
Matches 15; Conservative
                                                                                    APPLICANT: Cao, Yongwei
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US-10-260-708-82
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                                                                                                                                                  Query Match 100.0%; Score 80; DB 9; Length 377; Best Local Similarity 100.0%; Pred. No. 7.3e-05; Matches 15; Conservative 0; Mismatches 0; Indels
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020119463A1 1709118CD1
US-09-919-172-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 80; DB 15; Length 3' Best Local Similarity 100.0%; Pred. No. 7.3e-05; Matches 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 64, Application US/10236031B
Sequence 64, Application US/10236031B
Publication No. US20030219760A1
SEQUENCE INFORMATION:
APPLICANT: Gordon, Gavin J.
APPLICANT: Gullans, Steven R.
APPLICANT: Bueno, Raphael
TITLE OF INVENTION: Diagnostic and Prognostic TITLE OF INVENTION NUMBER: US/10/236,031B
CURRENT FILING DATE: 2002-09-05
PRIOR APPLICATION NUMBER: US 60/317,389
PRIOR PAPLICATION NUMBER: US 60/317,389
PRIOR PILING DATE: 2001-09-05
PRIOR FILING DATE: 2001-09-05
PRIOR FILING DATE: 2001-09-05
PRIOR APPLICATION NUMBER: US 60/407,431
PRIOR FILING DATE: 2002-06-30
                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-236-031B-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 15
US-10-236-031B-64
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Search completed: April 8, 2005, 12:50:57 Job time: 42.6667 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

April 8, 2005, 09:58:56 ; Search time 9.3333 Seconds (without alignments) 154.634 Million cell updates/sec Run on:

US-09-423-351C-2 80 Title: Perfect score:,

1 FPSIVGRPRHQGVMV 15 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:* Database :

pirl: * pir2: * pir3: * .....

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		•			SUMMARIES	
Result No.	Score	Query Match	Length	DB	ID	Description
1	80	100.0	98	2	C43616	actin beta, cytoso
7	80	100.0	137	7	A28258	5C - E
e	80	100.0	158	7	149465	alpha-cardiac acti
4	80	100.0	213	7	A61043	actin CA15 - sea s
ß	80	100.0	308	(7)	A03000	
9	80	100.0	328	7	S05430	actin beta - grass
7	80	100.0	349	N	B25819	actin, fetal skele
œ	80	100.0	362	7	A26559	actin type 5, cyto
6	80	100.0	374	П	ATBOB	actin beta - bovin
10	80	100.0	374	П	ATBOG	actin gamma - bovi
11	80	100.0	374	~	JC5818	gamma-actin - huma
12	80	100.0	375	7	ATBOSM	actin, aortic smoo
13	80	100.0	375	7	ATRB	
14	80	100.0	375	7	ATRIC	actin beta - rat
15	80	100.0	375	٦	A48324	actin beta, cytosk
16	80	100.0	375	ч	ATCHB	actin beta - chick
17	80	100.0	375	ч	ATHUB	actin beta - human
	80	100.0	375	Н	ATHUG	actin gamma 1 - hu
19	80	100.0	375	Ч	ATMSB	actin beta - mouse
	80	100.0	375	7	ATMSG	actin gamma - mous
21	80	100.0	375	-	ATRBB	actin beta, non-mu
	80	100.0	375	٦	S11222	actin gamma, cytos
23	80	100.0	375	~	S33386	actin, cytosolic (
	80	100.0	375	7	T25272	hypothetical prote
25	80	100.0	375	~	S71125	•
56	80	100.0	375	~	S71124	actin beta-1, cyto
27	80	100.0	375	N	S71126	actin beta, cytoso
28	80	100.0	375	~	A55001	beta -
59	80	100.0	375	7	A54728	actin alpha, cardi

actin - Phaffia rh	actin 7 - fruit fl	actin gamma, cytos	actin gamma, smoot	actin 8 - fruit fl	actin CyI - sea ur	Actin-1A - nematod	actin 87E - fruit	actin - fruit fly	actin, cytosolic -	actin, muscle - st	actin 15A - sea ur	actin - sea urchin	actin gamma, enter	actin - Hydra atte	actin (clone gen3)
S70377	ATFF7	A43552	ATCHSM	ATFF8	ATURS	A48449	S04538	JC1246	JS0189	JS0190	S07288	S09578	A40261	JQ0154	JN0832
N	-	-	-	-	Н	7	~	~	N	~	~	N	~	~	~
375	376	376	376	376	376	376	376	376	376	376	376	376	376	376	376
100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
80	80	80	80	80	80	80	80	80	80	80	80	80	80	80	80
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

#### ALIGNMENTS

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catin beta, cytosolic - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: ll-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 09-Jul-2004
C;Accession: C43616
R;Paterson, B.M.; Eldridge, J.D.
Science 224, 1436-1438, 1384
A;Title: alpha-Cardiac actin is the major sarcomeric isoform expressed in embryonic avia A;Reference number: A43616; MUID:84223949; PMID:6729461
A;Accession: C445616
A;Accession: C445616
A;Accession: C445616
A;Accession: C445616
A;Accession: C45616
A;Accession: C45616
A;Cross-references: UNIPROT:Q90736; GB:K02173; NID:g211054; PIDN:AAA98513.1; PID:g211055
C;Superfamily: actin
C;Keywords: cytosol; methylated amino acid
F;73/Modified site: 3'-methylhistidine (His) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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Best Local Similarity 100.0
Matches 15; Conservative
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# 31 FPSIVGRPRHQGVMV 45 1 FPSIVGRPRHQGVMV 15

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RESULT 2

cycles. Sc. fruit fly (Drosophila melanogaster)

cycles: Drosophila melanogaster

cycles: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004

cyclession: A28258

cycless A;Cross-references: UNIPROT:P10987 A;Note: the authors translated the codon GAG for residue 96

as Gly

C, Genetics:

A;Gene: FlyBase:Act5C A;Cross-references: FlyBase:FBgn0000042 C;Superfamily: actin C;Keywords: methylated amino acid F;74/Modified site: 3'-methylhistidine (His) #status predicted

100.0%; Score 80; DB 2; Length 137; 100.0%; Pred. No. 1.2e-06; Query Match Best Local Similarity

Matches

g

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C;Accession: A03000
R;Fyrberg, E.A.; Bond, B.J.; Hershey, N.D.; Mixter, K.S.; Davidson, N.
C[1] 24, 107-116, 1981
A;Title: The actin genes of Drosophila: protein coding regions are highly conserved but : A;Reference number: A03000; MUID:81210174; PMID:6263481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RiAlonso, S.; Minty, A.; Bourlet, Y.; Buckingham, M.
J. Mol. Evol. 23, 11-22, 1986
A;Title: Comparison of three actin-coding sequences in the mouse; evolutionary relations!
A;Reference number: A25819; MUID:86200234; PMID:3084797
A;Accession: B25819.
                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-308 <FYR>
A;Residues: 1-308 <FYR>
A;Cross-references: UNIPROT:P02572
A;Note: there are 68 unsequenced residues between positions 160 and 161. Partial sequence A;Note: the authors translated the codon GTT for residue 263 as Ile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rillu, Z.; Zhu, Z.; Roberg, K.; Faras, A.J.; Guise, K.S.; Kapuscinski, A.R.; Hackett, P. Nucleic Acids Res. 17, 5850, 1989
A;Title: The beta-actin gene of carp (Ctenopharyngodon idella).
A;Reference number: S05430; MUID:89345185; PMID:2762162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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C;Species: Ctenopharyngodon idella (grass carp)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Mus musculus (house mouse)
C;Date: 23-Aug-1987 #sequence_revision 23-Aug-1987 #text_change 09-Jul-2004
C;Accession: B25819
                                  C.Species: Drosophila melanogaster
C.Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
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C;Superfamily: actin
C;Keywords: cytoskeleton; methylated amino acid
C;Keywords: cytoskeleton; methylatedine (His) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Superfamily: actin
C;Keywords: methylated amino acid
F;74/Modified site: 3'-methylhistidine (His) #status predicted
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    fruit fly (Drosophila melanogaster) (fragments)

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100.0%; Score 80; DB 2; L
Best Local Similarity 100.0%; Pred. No. 2.8e-06;
Matches 15; Conservative 0; Mismatches 0;
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; Pred. No. 3e-06;
0; Mismatches 0
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A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-328 <LIU>
A;Cross-references: UNIPROT:P83751; EMBL:M25013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Genetics:
A;Gene: FlyBase:Act42A
A;Cross-references: FlyBase:FBgn0000043
A;Map position: 42A
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Best Local Similarity 100.0%;
Matches 15; Conservative 0
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: 149466; 149466
R;Garner, 1.; Minty, N.J.; Alonso, S.; Barton, P.J.R.; Buckingham, M.E.
EMBO J. S; 2559-2567, 1986
A;Title: A 5' duplication of the alpha-cardiac actin gene in BALB/c mice is associated A;Reference number: 149465; MUID:87053822; PMID:3023046
A;Accession: 149465
A;Accession: 149465
A;Accession: 149465
A;Residues: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-158 cRES
A;Cession: 149466
A;Accession: 149466
A;Acce
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C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession A61043
R;Beach, R.L.; Jeffery, W.R.
Dev. Genet. 11, 2-14, 1990
Dev. Genet. 11, 2-14, 1990
A;Title: Temporal and spatial expression of a cytoskeletal actin gene in the ascidian St
A;Reference number: A61043; MUID:90298580; PMID:2361333
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A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-213 < BEB.>
A;Cross-references: UNIPROT:Q7M3Y7
C;Comment: This sequence is expressed in cells undergoing rapid cell division.
C;Superfamily: actin
C;Keywords: cytoskeleton; methylated amino acid; mitosis; structural protein
F;73/Modified site: 3'-methylhistidine (His) #status predicted
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           Gaps
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100.0%; Score 80; DB 2; Length 21
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No.
           Mismatches
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Best Local Similarity 100.0
Matches 15; Conservative
               15; Conservative
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actin, aortic smooth muscle - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Jun.1987 #sequence_revision 30-Jun-1987 #text_change 06-Sep-1996
C;Accession: A02997; S13480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 80; DB 2; I 100.0%; Pred. No. 3.5e-06;
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A;Experimental source: monocyte
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                             FPSIVGRPRHQGVMV 15
                                                                   30 FPSIVGRPRHQGVMV 44
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Best Local Similarity 100.0
Matches 15; Conservative
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A;Residues: 1-374 <VANA.
A;Cross-references: UNIPROT:P60712
A;Note: only peptides that differed in composition from the corresponding peptides of ra
R;Degen, J.L.; Neubauer, M.G.; Degen, S.J.F.; Seyfried, C.B.; Morris, D.R.
B;Degen, J.L.; Morbauer, M.G.; Degen, S.J.F.; Seyfried, C.B.; Morris, D.R.
A;Title: Regulation of protein synthesis in mitogen-activated bovine lymphocytes. Analys
A;Reference number: A39105; MUID:84032385; PMID:6195151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Title: Actin mino-acid sequences. Comparison of actins from calf thymus, bovine brain A;Reference number: A14185; MUID:79045349; PMID:213279
A;Accession: E14185
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                        UNIPROT: Q61275; GB:X03767; GB:J00381; GB:M10652; NID:g49869; PIDN:CA
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A.Molecule type: mRNA
A.Residues: 76-227;344-374 <DEG>
A.Cross-references: GB:K00622; GB:K00623
A.Note: actins beta and gamma were not distinguished in this study
C.Comment: Vertebrate nonmuscle cells contain two highly conserved cytoskeletal actins,
                     A;Cross-references: UNIPROT:Q61275; GB:X03767; GB:J00381; GB:M10652; NID:g49869; 1S.Superfamily: actin
C;Superfamily: actin
C;Keywords: cardiac muscle; heart; methylated amino acid; muscle; skeletal muscle
F;47/Modified site: 3'-methylhistidine (His) #status predicted
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C;Date: 30-Sep-1991 #sequence revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: E141885, A39105; Ā02999; A14185
Evr. J. Biochem. 90, 451-462, 1978
                                                                                                                                                                                                                                                                                                                                                                                                                                           actin type 5, cytosolic - chicken
C;Species: Gallus gallus (chicken)
C;Date: 09-Sep-1987 #sequence_revision 09-Sep-1987 #text_change 05-Dec-1997
C;Accession: A26559
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                                                                                                                                                 Query Match 100.0%; Score 80; DB 2; Length 349; Best Local Similarity 100.0%; Pred. No. 3.2e-06; Matches 15; Conservative 0; Mismatches 0; Indels
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(S,Superfamily: actin
C;Keywords: cytosol; methylated amino acid
F;74/Modified site: 3.-methylhistidine (His) #status predicted
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R; Bergagma, D.J.; Chang, K.S.; Schwartz, R.J.
Mol. Cell. Biol. 5, 1151-1162, 1995
A; Reference number: A26559; MUID:85213487; PMID:4000121
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Best Local Similarity 100.0%;
Matches 15; Conservative 0
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A;Residues: 1-349 <ALO>
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                                                                                                                                                    Query Match
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Gaps

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Length 374; Indels

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R;Vandekerckhove, J.; Weber, K.
Eur. J. Biochem. 90, 451-462, 1978
A;Title: Actin amino-acid sequences. Comparison of actins from calf thymus, bovine brain
A;Reference number: A14185; WUID:79045349; PMID:213279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C. Reywords: Dicked amino end; cell motility; cytoskeleton; methylated amino acid; micro F_11/Modified site: blocked amino end (Glu) (probably acetylated) #status experimental F_172/Modified site: 3'-methylhistidine (His) #status predicted
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Cispecies: Homo sapiens (man)
Cibate: 20-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 09-Jul-2004
Cibate: 20-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 09-Jul-2004
Cisconsion: 405818; PC4501
R;Hauschildt, S.; Schwarz, C.; Heine, H.; Ulmer, A.J.; Flad, H.D.; Rietschel, E.T.; Jens Biochem: Biophys Res. Commun. 241, 670-674, 1997
A;Hitle: Actin: A target of lipopolysaccharid-induced phosphorylation in human monocytes A;Reference number: JC5818; MUID:98096379; PMID:9414766
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A;Residues: 1-61;84-112;147-190;196-209;215-253;335-358 <HA2>
A;Experimental source: monocyte
C;Comment: This protein is involved in a signal transduction that eventually leads to mo
C;Superfamily: actin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Note: only peptides that differed in composition from the corresponding peptides of ra
C,Comment: Vertebrate nonmuscle cells contain two highly conserved cytoskeletal actins,
C,Superfamily: actin
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actin gamma - bovine (tentative sequence)
C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
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muscle contraction

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Gaps

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A; Molecule type: DNA
A; Residues: 1-375 <LIU>
A; Cross-references: UNIPROT:P83750; GB:MZ4113; NID:g213041; PIDN:AAA68886.1; PID:g213042
A; Note: the authors translated the codon TTC for residue 21 as Pro, AAG for residue 50 a
7 as Pro
                                                                                                                                                                                             A; Title: The covalent maleimidobenzoyl-actin-myosin head complex. Cross-linking of the 5 A; Reference number: S44393; MUID:94259162; PMID:8200441
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C;Keywords: cell motility; cytoskeleton; methylated amino acid; microfilament; mitosis;
F;2-375/Product: actin beta #status predicted <AMT>
F;73/Modified site: 3'-methylhistidine (His) #status predicted
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A;Cross-references: GB:J00691; NID:g202653; PIDN:AAA40657.1; PID:g202654
C;Comment: Vertebrate nonmuscle cells contain two highly conserved cytoskeletal actins,
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R;Liu, Z.; Zhu, Z.; Roberg, K.; Faras, A.; Guise, K.; Kapuscinski, A.R.; Hackett, P.B.
DNA Seq. 1, 125-136, 1990
A;Title: Isolation and characterization of beta-actin gene of carp (Cyprinus carpio).
A;Reference number: A48324; MUID:92190540; PMID:2134183
A;Accession: A48324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-Jun-1983 #sequence_revision 13-Jun-1983 #text_change 22-Jun-1999
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C;Species: Cyprinus carpio (common carp)
C;Date: 03-Reb-1994 #sequence_revision 11-Apr-1997 #text_change 09-Jul-2004
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R.Nudel, U.; Zakut, R.; Shani, M.; Neuman, S.; Levy, Z.; Yaffe, D.
Nucleic Acids Res. 11, 1759-1771, 1983
A.Title: The mucleotide sequence of the rat cytoplasmic beta-actin gene.
A, Fitle: The mucleotide sequence of the rat cytoplasmic beta-actin gene.
A, Reference number: A38571; MUID:83168920; PMID:6300777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Keywords: acerylated amino end; ATP binding; methylated amino acid; E;1.75/Product: actin #status experimental (MAT>
F;1/Modified site: acetylated amino end (Asp) #status experimental F;73/Modified site: 3 -methylhistidine (His) #status experimental F;73/Modified site: 3 -methylhistidine (His) #status experimental
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100.0%; Pred. No. 3.5e-06;
iive 0; Mismatches 0;
                                                                                                        Ribertrand, R.; Derancourt, J.; Kassab, REBS Lett. 345, 113-119, 1994
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Best Local Similarity 100.
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A; Access
R; Vandekerckhove, J.; Weber, K.

Differentiation 14, 123-133, 1979
A; Title: The complete amino acid sequence of actins from bovine aorta, bov tiation.

A; Reference number: A02997; MUID:80047657; PMID:499690
A; Rolecule type: protein
A; Rolecule type: protein
A; Residues: 1-375 «VAN»
A; Residues: 40-49 «ZEV»
A; Residues: 40-40 «ZEV»
A; Residues: 40-40 «ZEV»
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N,Alternate names: F-actin
N,Alternate names: F-actin
S,Speciaes: OryColagus cuniculus (domestic rabbit)
C,Speciaes: OryColagus cuniculus (domestic rabbit)
C,Date: 30-Sep-1991 #sequence revision 30-Sep-1991 #text change 07-May-1999
C,Accession: A92182; A14185; $65873; $70610; $44393; A02994
R,Collins, J.H.; Blzing, M.
J Biol. Chem. 250, 5915-5920, 1975
A,Fithe: The primary structure of actin from rabbit skeletal muscle. Completion and anal A,Reference number: A92182; MUID:75211334; PMID:1150665
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A, Molecule type: protein
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C;Comment: Vertebrate nonmuscle cells contain two highly conserved cytoskeletal actins, C;Genetics:
A;Introna.
A;Introna.
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C;Genetics:
C;Genetics:
C;Superfamily: actin
C;Keywords: acetylated amino end; cell motility; cytoskeleton; methylated amino acid; mi
F;2.375/product: actin beta, cytoskeletal #setaus predicted cMATS-
F;2.776/modified site: acetylated amino end (App) (in mature form) #status predicted
F;7.7/Modified site: 3'-methylhistidine (His) #status predicted
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ö penaeus van lotharella lotharella styela clav oxyuranus s lotharella homo sapien anopheles g chlorarachn musculu lotharella lotharella lotharella 25-0CT-2004 (TrEMBLrel. 28, Created)
25-0CT-2004 (TrEMBLrel. 28, Last sequence update)
25-0CT-2004 (TrEMBLrel. 28, Last annotation update)
25-0CT-2004 (TrEMBLrel. 28, Last annotation update)
25-0CT-2004 (TrEMBLrel. 28, Last annotation update)
Cytoplasmic actin (Fragment).

Bombyx mori (Silk moth).

Bombyx mori (Silk moth).

Bombycota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Bombycidae; Bombyx.

MCBI _TaxIb=7091; Gaps Beta actin (Fragment). Ovis aries (Sheep). Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; ö 07m3y7 064g13 07xb23 07xb24 07xb24 07xb21 07xb20 07xb20 07xb20 07xb20 07xb20 100.0%; Score 80; DB 2; Length 26; 100.0%; Pred. No. 8.2e-07; ive 0; Mismatches 0; Indels Last sequence update) Last annotation update) 53 AA. 26 AA ALIGNMENTS Created) Q810R5 Q6ZYL2 Q7M3Y7 Q64G13 Q7XB23 Q7XB24 Q7XB25 Q6RXK3 Q7XB21 Q7XB22 Q7XB20 Q7XB28 Q7Z7J6 PRT; PRT; Q6Q298; 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 1 FPSIVGRPRHQGVMV 15 15; Conservative PRELIMINARY; PRELIMINARY; Local Similarity NCBI_TaxID=9940; Caprinae; 000000000000000 Query Match RESULT 1 Q6Q298 ID Q6Q298 Q6AW41; **Q6AW41** Best Loca Matches RESULT 2 ઠે 셤 

SEQUENCE FROM N.A.
STRAIN=Daizo; TISSUE=Silk gland;
Shiomi K., Kajiura Z., Nakagaki M., Yamashita O.;
Baculovirus-mediated efficient gene transfer into the central nervous system of the silkworm, Bombyx mori.";
Nihon Sanshigaku Zasshi 72:149-155(2003).

[2] SEQUENCE FROM N.A.

STREETS

RESULT 3 O61375

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Schmidtea polychroa.
Bukaryota, Metazoa, Platyhelminthes; Turbellaria; Seriata; Tricladida;
Paludicola; Dugesiidae; Schmidtea.
                      Platyhelminthes; Turbellaria; Seriata; Tricladida;
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GO; GO:0003774; F:motor activity; IEA.
GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
                                                                                                                                                                                                                                                         GO: GO:0005884; C:actin filament; IEA.
GO: GO:0003774; F:motor activity; IEA.
GO: GO:0005200; F:structural constituent of cytoskeleton; IEA.
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Last annotation update)
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100.0%; Pred. No. 2.7e-06;
tive 0; Mismatches 0;
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                     Eukaryota, Metazoa, Platyhelminthe
Paludicola, Dugesiidae, Schmidtea.
NCBI_TaxID=50054;
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InterPro; IPR004000; Actin_like.
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InterPro; IPR004000; Actin_like.
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PROSITE; PS00406; ACTINS_1; 1.
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PROSITE; PS00406; ACTINS_1; 1.
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            Schmidtea polychroa.
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es 15; Conserv
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SEQUENCE FROM N.A.
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061377;
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Bukaryota, Metazoa, Platyhelminthes; Turbellaria; Seriata; Tricladida;
Paludicola; Dugesiidae; Schmidtea.
NCBI_TaxID=50054;
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"Multiple isoform recovery (MIR)-PCR: a simple method for the
"Multiple isoform recovery (MIR)-PCR: a simple method for the
isolation of related mRNA isoforms.";
Nucleic Acids Res. 26:2031-2033(1998).
-!- FUNCTION: Actins are highly conserved proteins that are involved
in various types of cell motility and are ubiquitously expressed
in all eukaryotic cells (By similarity).
-!- SIMILARITY: Belongs to the actin family.
-!- SIMILARITY: AAC38981.1;
-- HSSP; PO2577; INM1.
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GO; GO:0003774; F:motor activity; IEA.
GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
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                                                                                                                           100.0%; Score 80; DB 2; Length 53; 100.0%; Pred. No. 1.8e-06; Live 0; Mismatches 0; Indels
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Pred. No. 2.7e-06;
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            Shiomi K.;
Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AB186491; BAD35130.1; -.
InterPro; IPR004000; Actin_like.
Pfam; PF00022; Actin; 1.
NON TER
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                                                                                                 SEQUENCE 53 AA; 5465 MW; 227AA8B4872EBA86 CRC64;
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(TrEMBLrel. 07, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
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InterPro, IPR004000; Actin_like.
STRAIN=Daizo; TISSUE=Silk gland;
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Name=DpAct1;
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Best Local Similarity
Matches 15; Conserv
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RESULT 4 061376 ID 0613 AC 0613 DT 01-A DT 01-G DT 01-G

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Length 78; Indels

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RESULT 6 Q95183

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Paterson B.M., Eldridge J.D.;

"alpha-Cardiac actin is the major sarcomeric isoform expressed in malpha-Cardiac actin is the major sarcomeric isoform expressed in embryonic avian skeletal muscle.";

Science 224:1436-1436|1984].

-!- FUNCITON: Actins are highly conserved proteins that are involved in various types of cell motility and are ubiquitously expressed in all eukaryotic cells (By similarity).

EMBL; KO1713; AAA98513.1;

EMBL; KO173; AAA98513.1;

R PIR; C43616; C34516.

R PSSP; PO2577; 1NM1.

GO GO:0005840; C:actin filament; IEA.

R GO; GO:0005840; F:structural constituent of cytoskeleton; IEA.
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McGowan C., Davidson E.A., Davidson W.S.;
Submitted (MAR-2013) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Actins are highly conserved proteins that are involved in various types of cell motility and are ubiquitously expressed in all eukaryotic cells (By similarity).
-!- SIMILARITY: Belongs to the actin family.
HSSP; P02577; INMI.
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Salvelinus alpinus (Arctic char).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Salvelinus.
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GO; GO:0003774; F:mctor activity; IEA.
GO; GO:0005200; F:mctoural constituent of cytoskeleton; IEA.
InterPro; IPR004001; Actin.
InterPro; IPR004000; Actin.like.
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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                                SEQUENCE FROM N.A.
MEDLINE=84223949; Pubmed=6729461;
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PROSITE; PS00406; ACTINS_1; 1.
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Pfam; PF000022; Actin, 1.
PRINTS; PR00190; ACTIN.
PROSITE; PS00406; ACTINS_1; 1.
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Matches 15; Conservative
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NON_TER 91 SEQUENCE 91 AA; 10
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NCBI_TaxID=9031;
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01-NOV-1996 (TrEMBirel. 01, Last sequence update)
01-NUV-1993 (TrEMBirel. 24, Last annotation update)
01-JUN-2003 (TrEMBirel. 24, Last annotation update)
Beta-actin (Fragment).
Gallus gallus (Chicken).
Gallus gallus (Chicken).
Archosauria; Aves; Neognathae; Craniata; Phasianidae; Phasianiae;
Gallus.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
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GO; GO:0003774; F:mctor activity; IEA.
GO; GO:0003770; F:mtructural constituent of cytoskeleton; IEA.
InterPro; IPR004000; Actin.
InterPro; IPR004000; Actin_like.
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MEDLINE=22306422; PubMed=12388084;
Mang D.-A., Du H., Jaggar J.H., Brindley D.N., Tigyi G.J.,
Watsky M.A.;
                                                                   Length 78;
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                78 78 78 78 78 78 AA; B9DFF1108E4ADB0E CRC64;
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Beta-actin (Fragment).
                                                                   100.0%; Score 80; DB 2; I 100.0%; Pred. No. 2.7e-06;
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Pred. No. 2.7e-06;
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PROSITE; PS00406; ACTINS_1; 1.
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01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
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Matches
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BEDLINE=22480340.7; PubMed=12574518; DOI=10.1073/pnas.0336368100;
Wittkopp P.J., Williams B.L., Selegue J.E., Carroll S.B.;
"Drosophila pigmentation evolution: divergent genotypes underlying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.
NCBI_TaxID=47314;
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Pred. No. 3.3e-06;
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96 AA; 10610 MW; 1454B7D9DD3F3564 CRC64;
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100.0%; Pre
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InterPro; IPR004000; Actin_like.
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PROSITE; PS00406; ACTINS_1; 1.
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01-JUN-2003 (TrEMBLrel. 24,
01-MAR-2004 (TrEMBLrel. 26,
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                                          1 FPSIVGRPRHQGVMV 15
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Matches 15; Conservative
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                                                                                 29 FPSIVGRPRHQGVMV
                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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Buelow H.E., Bernhardt R.;
Buelow H.E., Bernhardt R.;
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Actins are highly conserved proteins that are involved in various types of cell motility and are ubiquitously expressed in all eukaryotic cells (By similarity).
-!- SIMILARITY: Belongs to the actin family.
EMBL; AR191277; AAF19237;
HSSP; PO2577; LNM1.
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                                                                              Convergent phenotypes.;
Proc. Natl. Acad. Sci. U.S.A. 100:1808-1813(2003)
-!- FUNCTION: Actins are highly conserved proteins that are involved in various types of cell motility and are ubiquitously expressed in all eukaryotic cells (By similarity).
-!- SIMILARITY: Belongs to the actin family.
HiSSP; P02568; ILCU.
MEDLINE=22480340; PubMed=12574518; DOI=10.1073/pnas.0336368100; Wittkopp P.J., Williams B.L., Selegue J.E., Carroll S.B.; "Drosophila pigmentation evolution: divergent genotypes underlying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
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G0; G0:0003774; F:motor activity; IEA.
G0; G0:0003774; F:motor activity; IEA.
G0; G0:0003770; F:structural constituent of cytoskeleton; IEA.
InterPro; IPR004001; Actin.
InterPro; JPR004001; Actin.
FFam; PF00022; Actin; 1.
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GO; GO: 0003774; F:motor activity; IEA.
GO; GO: 0001274; F:motor activity; IEA.
InterPro; IPRO0401; Actin_like.
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Pred. No. 3.3e-06;
Mismatches 0; Indels
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01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNAY-2003 (TrEMBLrel. 24, Last annotation update)
Cytoplasmic actin (Fragment)
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"R PROSITE; PR00190; ACTIN. 1.
"R PROSITE; PS00406; ACTINS_1; 1.
"Y Structural procein.
"NON TER 99 ° SEQUENCE a°
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PROSITE; PS00406; ACTINS_1; 1.
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100.0%;
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Best Local Similarity 100...
And 15; Conservative
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Q86SB7 Q86SB7;

RESULT 12 Q86SB7

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SEQUENCE FROM N.A.

MEDLINE=9733945; PubMed=9190067;

Kissinger J.C., Hahn J.H., Raff R.A.;

Rapid evolution in a conserved gene family. Evolution of the actin gene family in the sea urchin genus Heliocidaris and related genera.";

Mol. Biol. Evol. 14:654-665(1997).

-!- FUNCTION: Actins are highly conserved proteins that are involved in various types of cell mollity and are ubiquitously expressed in all enkaryotic cells (By similarity).

-!- SIMILARITY: Belongs to the actin family.
-!- FUNCTION: Acting are highly conserved proteins that are involved in various types of cell motility and are ubiquitously expressed in all eukaryotic cells (By similarity).
-!- SIMILARITY: Belongs to the actin family.
EMBL; UR5542; AAB66299.1; --
HSSP; P10983; 1D4X.
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Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Temnopleuroida; Toxopneustidae;
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                                                                                                                                                                             GO; GO:0005884; C:actin filament; IEA.
GO; GO:0003774; F:motor activity; IEA.
GO; GO:00003700; F:motoural constituent of cytoskeleton; IEA.
Interpro; IPR00401; Actin.
InterPro; IPR004000; Actin.like.
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100.0%; Pred. No. 3.8e-06;
tive 0; Mismatches 0;
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Pred. No. 3.8e-06;
; Mismatches 0;
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PRINTS; PR00190; ACTIN.
PROSITE; PS00406; ACTINS_1; 1.
PROSITE; PS01132; ACTINS_ACT_LIKE; 1.
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PROSITE; PS01132; ACTINS_ACT_LIKE; 1.
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InterPro; IPR004000; Actin_like.
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Best Local Similarity 100.0
Matches 15; Conservative
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PRINTS; PR00190; ACTIN.
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NON TER 108 1C
SEQUENCE 108 AA; 1
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NON_TER 108 10
SEQUENCE 108 AA;
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Best Local Similarity
Matches 15; Conserv
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MEDLINE=97333945; PubMed=9190067;
Kissinger J.C., Hahn J.H., Raff R.A.;
Rapid evolution in a conserved gene family. Evolution of the actin gene family in the sea urchin genus Heliocidaris and related genera.";
Mol. Biol. Evol. 14:654-665(1997).
                                                                                                                                                                                                                                                                                                                                                                                          Gryllus bimaculatus (Two-spotted cricket).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllidae; Gryllinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zhang H., Shinmyo Y., Hirose A., Mito T., Inoue Y., Ohuchi H.,
Loukeris T.G., Noji S.,
Loukeris T.G., Noji S.,
Extrachromosomal transposition of the transposable element Minos
occurs in embryos of the cricket Gryllus bimaculatus.";
Dev. Growth Differ. 0:0-0(2002)
-:- FUNCTION: Actins are highly conserved proteins that are involved
in various types of cell motility and are ubiquitously expressed
in all eukaryotic cells (By similarity).
-:- SIMILARITY: Belongs to the actin family.
EMBL; AB087882; BAC55093.1; --
HSSP; PO2577; 1NM1.
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Eukaryota, Metazoa, Echinodermata, Eleutherozoa, Echinozoa,
Echinoidea, Euechinoidea, Echinacea, Temnopleuroida, Toxopneustidae,
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GO; GO:0003774; F:motor activity; IEA.
GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
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                                                                                                                                                                                                                                     01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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InterPro, IPR004000; Actin_like
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PROSITE; PS00406; ACTINS_1; 1.
   31 FPSIVGRPRHQGVMV 45
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hes 15; Conservative
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                                                                                                                                                                                                                                                                                                                                  Actin (Fragment).
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01-JAN-1998
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SEQUENCE Query Match

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RESULT 13 018548

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1. FUNCTION: Actina are highly conserved proteins that are involved in various types of cell motility and are ubiquitously expressed in all enkaryotic cells (By similarity).

1. SIMILARITY: Belongs to the actin family.

EMBL; ATLIGS36; AAM66751.1; -
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2002 (TrEMBLrel. 24, Last annotation update)
01-0TUN-2003 (TrEMBLrel. 24, Last annotation update)
Beta-actin (Fragment).
Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
Actinopterygii, Neopterygii, Teleostei; Euteleostei; Neoteleostei;
Acanthomocrpha, Acanthopterygii; Percomorpha; Perciformes; Labroidei;
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GO; GO:0005884; C:actin filament; IEA.

GO; GO:0005774; F:moctor activity; IEA.

GO; GO:005200; F:structural constituent of cytoskeleton; IEA.

InterPro; IPR004001; Actin.

InterPro; IPR004000; Actin.like.
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Pred. No. 4.2e-06;
Mismatches 0; Indels
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NON TER 121 121
SEQUENCE 121 AA; 13458 MW; 04A58F271BBA0898 CRC64;
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100.0%; Pred. No....
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PRINTS; PR00190; ACTIN.
PROSITE; PS00406; ACTINS_1; 1.
PROSITE; PS01132; ACTINS_ACT_LIKE; 1.
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1 FPSIVGRPRHQGVMV 15
                                           18 FPSIVGRPRHQGVMV 32
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Best Local Similarity 100.
Matches 15; Conservative
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NCBL TaxID=8128;
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-423-351C-3 82 1 GRPRHQGVMVGMGQK 15 Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

2105692 seqs, 386760381 residues Searched: Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB M Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp1980s:*
geneseqp1990s:*
geneseqp2000s:*
geneseqp2001s:* A_Geneseq_16Dec04:* Database :

geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp20048:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

		d			STANTAGE			
Result No.	Score	Query Match	Length	DB	ID		Description	по
	82	100.0	15	5	AAW92529		Aaw92529	Beta-acti
7	82	100.0	19	N	AAW92543		Aaw92543	Beta-acti
e	82	100.0	105	ហ	ABP42469		Abp42469	Human ova
4	82	100.0	157	4	ABB66853		Abb66853	Drosophil
S	82	100.0	201	ഹ	ABP43176		Abp43176	Human ova
9	82	100.0	204	ഹ	ABP43016		Abp43016	Human ova
7	82	100.0	310	ω	ADR38362		Adr38362	pigA3Cy3G
ω	82	100.0	342	7	ADM05323		Adm05323	Human pro
6	82	100.0	374	m	AAB12985		Aab12985	Human bet
10	82	100.0	375	Н	AAP61532		Aap61532	Sequence
11	82	100.0	375	~	AAR50328		Aar50328	Drug resi
12	82	100.0	375	m	AAB15017		Aab15017	Posttrans
13	82	100.0	375	ო	AAY94569		Aay94569	Human car
14	82	100.0	375	ო	AAB15016		Aab15016	Posttrans
15	82	100.0	375	Ŋ	ABB77395		Abb77395	Human act
16	82	100.0	375	9	ABR64271	,	Abr64271	Angiogene
17	82	100.0	375	9	ABM04830		Abm04830	Rat cytop
18	82	100.0	375	7	ADB85212		Adb85212	Rat actin
19	82	100.0	375	7	ADE61174		Ade61174	Rat Prote
20	82	100.0	375	7	ADF30525		Adf30525	Rat angio
21	82	100.0	375	7	ADI63062		Adi63062	Human apo
22	82	100.0	375	7	ADI62970		Adi62970	Нишап аро
23	82	100.0	375	7	ADI63040		Adi63040	Human apo
24	82	100.0	375	œ	ADL13002		Ad113002	Human ste
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## ALIGNMENTS

Peptide substrate; CCT; eukaryotic type II chaperonin complex; cyclin; binding agent; substrate-binding site; SBS; substrate folding; actin; tubulin; treatment; cancer; anticancer drug; viral infection; screening; Beta-actin reference peptide substrate #3. AAW92529 standard; peptide; 15 AA (first entry) reduced toxicity. 26-APR-1999 AAW92529; RESULT 1 AAW92529 

Synthetic.

WO9853322-A1

26-NOV-1998.

98WO-GB001485. 22-MAY-1998; 97GB-00010762. 23-MAY-1997; (CANC-) INST CANCER RES ROYAL CANCER HOSPITAL.

Liou AK; Hynes G, Willison K,

WPI; 1999-070162/06.

Identifying specific binding agents for substrate binding site in CCT chaperonin complex - also new peptide binding agents and their mimetics, and peptides containing a specific CCT binding site, used for treating cancer

Disclosure, Fig 10, 97pp, English.

This invention describes a method which uses the CCT (eukaryotic type II chaperonin) complex or part of it, for identifying a binding agent that can occupy a substrate-binding site (SBS) on the CCT complex. By binding to the CCT complex, the binding agents block an SBS so that biological activity of the CCT complex is affected, particularly its ability to fold substrates such as actin, tubulin and cyclin. The binding agents are useful for trearment of cancer, particularly when used in combination with an anticancer drug, or viral infections. Nucleic acid fragments are used to screen for agents, e.g. binding agents that modulate interaction between the CCT complex and a protein that is to be folded. The binding

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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide substrate, CCT, eukaryotic type II chaperonin complex, cyclin, binding agent, substrate-binding site, SBS, substrate folding, actin, tubulin, treatment, cancer, anticancer drug; viral infection; screening; reduced toxicity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identifying specific binding agents for substrate binding site in CCT chaperonin complex - also new peptide binding agents and their mimetics, and peptides containing a specific CCT binding site, used for treating
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agents may target cells that are actively synthesising tubulin etc. (unlike known microtubule-stabilising agents that affect all cells) should have reduced toxicity for normal cells. AAM92527-W92541 are peptide substrates used in the method of the invention
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                                                                                                                         Length 15;
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6.8e-07;
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                                                                                                                       Score 82;
Pred. No. 6
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                                                                                                                                                                                                                                                                                                                   AAW92543 standard; peptide; 19 AA.
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                                                                                                                                         Similarity
                                                                                      Sequence 15 AA;
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                                                                                                                     Query Match
Best Local 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and neurological
                                                                                                                                                                                                                                                                                                                                                                                    Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour; ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndrome; PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; infection; cardiovascular disorder; respiratory disorder; neurological disorder; gene therapy; chromosome mapping; forensic analysis; antibody preparation; cytostatic; immunomodulatory; neuroprotective; antibody preparation; cytostatic; immunomodulatory; neuroprotective; antiinflammatory; gynaecological; reproductive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also encompasses polypeptides 90% identical and polynucleotides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         invention relates to 2175 novel human ovarian antigens (ABP41054-
                                        Gaps
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                                        .
Length 19;
                                        Indels
100.0%; Score 82; DB 2; I
100.0%; Pred. No. 8.7e-07;
                                                                                                                                                                                                                                                                                                                                                        Human ovarian antigen HOCQG94, SEQ ID NO:3601.
                                           Mismatches
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                                                                                                                                                                                                                               ABP42469 standard; protein; 105 AA.
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                                                                                   1 GRPRHQGVMVGMGQK 15
                                                                                                                        GRPRHQGVMVGMGQK 19
                                                                                                                                                                                                                                                                                                               (first entry)
                                             Conservative
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                   Local Similarity
nes 15; Conserv
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                                                                                                                                                                                                                                                                      ABP42469;
  Query Match
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                                           Matches
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respiratory disorders, neurological disorders, gastrointestinal disorders
                         and urinary system disorders. Ovarian antigen polypeptides and polynucleotides may also be used in screening for compounds which modulate ovarian antigen expression or activity. The polynucleotides may further be used for gene therapy, chromosome mapping, in the identification of individuals and in forensic analysis, and the polypeptides may be used as food additives or to prepare antibodies useful in disease diagnosis, drug targeting and phenotyping. The present sequence represents a human ovarian antigen of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 105 AA;
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Gaps
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          Length 105;
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. 5.10-06;
0; Indels
         Score 82; DB
Pred. No. 5.16
; Mismatches
        Match 100.0%; So
Local Similarity 100.0%; Pourse 15; Conservative 0;
         Query Match
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Matches
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1 GRPRHQGVMVGMGQK 15 51 37 GRPRHÓGVMVGMGQK ઠે 셤

ABB66853 standard; protein; 157 AA. RESULT 4 **ABB66853** 

ABB66853; 

Drosophila melanogaster polypeptide SEQ ID NO 27351. (first entry) 26-MAR-2002

Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.

Drosophila melanogaster.

WO200171042-A2

27-SEP-2001

23-MAR-2001; 2001WO-US009231.

23-MAR-2000; 2000US-0191637P. 11-JUL-2000; 2000US-00614150

(PEKE ) PE CORP NY

Myers EW Li PWD, Venter JC, Adams M,

WPI; 2001-656860/75 N-PSDB; ABL10956 New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.

Disclosure; SEQ ID NO 27351; 21pp + Sequence Listing; English.

capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly invention relates to an isolated nucleic acid detection reagent from WIPO at ftp.wipo.int/pub/published_pct_sequences The

Sequence 157 AA;

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                                                       Gaps
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100.0%; Score 82; DB 4; Length 157; 100.0%; Pred. No. 7.7e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human ovarian antigen HVVCQ49, SEQ ID NO:4308.
                                                    Mismatches
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                                                                                                         1 GRPRHQGVMVGMGQK 15
                                                                                                                                                37 GRPRHQGVMVGMGQK 51
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                                                    15; Conservative
                           Best Local Similarity
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Query Match
                                                    Matches
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ABP43176
ID ABP4
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Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and neurological diseases

Birse CE, Rosen CA; 2002-147878/19.

N-PSDB; ABQ56253

Claim 11; SEQ ID NO 4308; 2922pp; English.

The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP4328) and to CDNAs encoding them (ABD54131-ABD563165), and also encompasses polypeptides 90% identical and polymucleotides 95% identical to the sequences of the invention. The invention additionally relates to combinant vectors and host cells comprising human ovarian antigens, and the use of ovarian antigens, antibodies against human ovarian antigens, and the use of ovarian polymucleotides and polypeptides in diagnosing, treating, prognosing or preventing various ovary and/or breast-related disorders Such conditions include ovarian cancer, and breast cancer, and castactic tumours of ovarian or breast origin, reproductive system disorders (e.g., infertility, disorders of pregnancy, anovulation, closucders, infertions (e.g., chlamydia, HIV, toxoplasmosis, and toxic shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and vaginted immundeficiencies, autoimmune ophoritis, systemic lupus erythematosus), clod-related disorders (e.g., anaemia), cardiovascular disorders, neurological disorders, gastrointestinal disorders

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and urinary system disorders. Ovarian antigen polypeptides and polynucleotides may also be used in screening for compounds which modulate ovarian antigen expression or activity. The polynucleotides may further be used for gene therapy, chromosome mapping, in the identification of individuals and in forensic analysis, and the bolypeptides may be used as food additives or to prepare antibodies useful in disease diagnosis, drug targeting and phenotyping. The present sequence represents a human ovarian antigen of the invention. Note: The specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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Pred. No. 9.9e-06;
Mismatches 0; Indels
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Best Local Similarity 100.
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1 GRPRHQGVMVGMGQK 15 53 GRPRHQGVMVGMGQK 67 RESULT 6 ABP4301 g à

ABP43016 standard; protein; 204 AA. (first entry) 22-AUG-2002 ABP43016; 

Human ovarian antigen HSPSB24, SEQ ID NO:4148.

Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour; ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anövulation; polycystic ovary syndrome; pcOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; infection; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disorder; urinary system disorder; drug screening; gene therapy; chromosome mapping; forensic analysis; antibody preparation; cytostatic; immunomodulatory; neuroprotective; antiinflammatory; gynaecological; reproductive.

Homo sapiens.

WO200200677-A1.

03-JAN-2002

07-JUN-2000; 2000US-0209467P

07-JUN-2001; 2001WO-US018569

(HUMA-) HUMAN GENOME SCI INC

Birse CE, Rosen CA;

2002-147878/19.

WPI; 2002-147878/ N-PSDB; ABQ56093

Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and neurological

Claim 11; SEQ ID NO 4148; 2922pp; English.

The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP43228) and to cDNAs encoding them (ABQ54131-ABD56305), and also encompasses polypeptides 90% identical and polynucleotides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigen

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polynucleotides, antibodies against human ovarian antigens, and the use of ovarian antigen polynucleotides and polypeptides in diagnosing, treating, prognosing or preventing various ovary and/or breast-related disorders. Such conditions include ovarian cancer and breast cancer, and metastatic tumours of ovarian or breast origin, reproductive system disorders (e.g., infertility, disorders of pregnancy, anovulation, colycyptic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and cyanintis), immune disorders (e.g., congenital and acquired immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus), blood-related disorders (e.g., angenital and acquired confirmaty system disorders. Ovarian antigen polypeptides and urinary system disorders. Ovarian antigen polypeptides and polynucleotides may also be used in screening for compounds which colymulate ovarian antigen expression or activity. The polynucleotides may be used an in screening for compounds which continue and individuals and in forensic analysis, and the cleantification of individuals and in forensic analysis, and the colypeptides may be used as food additives or to prepare antibodies cuseful in disease diagnosis, drug targeting and phenotyping. The present sequence tagenessents a human ovarian antigen of the invention. Note: The sequence data for this patent did not form part of the printed sequence. The proposition is the polymulation of the printed sequence data for this patent did not form part of the printed from a for mindividual or semments.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Introducing foreign gene into insect cell, involves introducing DNA having foreign gene integrated between inverted repeat sequences of piggyBac transposon and piggyBac transposase that acts on inverted repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pigA3Cy3GFP plasmid protein product (Cycle3 GFP under an actin promoter).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  piggyBac; transposon; transposase; gene transfer; plasmid; Cycle3 GFP; actin promoter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 82; DB 5; Length 204; 100.0%; Pred. No. 1e-05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       specification, but was obtained in electron at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADR38362 standard; protein; 310 AA.
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hes 15; Conservative
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Unidentified.
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RESULT 10
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                                                      into an insect cell. Specifically, it refers to a foreign gene occurring between inverted repeat sequences of a pigyBac transposon and using a pigyBac transposon and using a pigyBac transposon and using a reflictency. The present invention describes the insect cell as that of lepidoptera insect origin, preferably it is the silk worm Bombyx mori, and stable integration occurs into the genome of this insect using the transposace enzyme. In particular, this gene transfer method uses the planmid pigA3Cy3GFP which contains a Cycle3 GFP gene expressed under a sequences of the transposace or promoter; between a pair of inverted repeat sequences of the transposace or pigA3Cy3GFP plasmid DNA that represents the protein promoter controlling expression of the Cycle3 GFP gene given in an exemplification of the invention. NOTE: This sequence is the control of the invention. NOTE: This sequence is the control of the invention. NOTE: This sequence is
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?, Tamechika I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a novel human polynucleotide and the encoded polypeptide. A polynucleotide of the invention may have a use in gene therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful as a primer for synthesizing the polynucleotide or as a probe for
                                                This invention relates to a novel method for introducing a foreign gene
                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in gene therapy,
regulating their
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Hio Y, Otsuka K, Nagai K, Irie R,
Otsuka M, Nagahari K, Masuho Y;
                                                                                                                                                                                                                                                                                  Length 310;
                                                                                                                                                                                                                                                                      Score 82; DB 8; Length sire Pred. No. 1.5e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polynucleotides and polypeptides are useful in gene developing a diagnostic marker or medicines for regulat: expression and activity, or as a target of gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human; gene therapy; diagnostic marker; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human protein of the invention SEQ ID NO:4008.
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                       Disclosure; Page; 25pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                   1 GRPRHQGVMVGMGQK 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                           GRPRHQGVMVGMGQK
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Yoshikawa T,
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Best Local Similarity
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                                                                                                                                                                                                                                                           Sequence 310 AA;
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Seki N, Yos
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 sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Treatment for sickle cell anemia comprises administering a reducing agent to inhibit and reverse sickled cell formation in blood.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention provides a treatment for sickle cell anaemia, which comprises administering a reducing agent. The treatment inhibits the formation of irreversible sickled cells (ISC) and reverses ISC formation in the blood. The present sequence represents the human beta-actin protein. The sequence is used in the invention to demonstrate that a disulphide bridge is formed between cystelines 284 and 373 in ISC beta-actin as a post-translational modification. The reducing agent used in the treatment acts to correct this post-translational modification
detecting the polynucleotide. The polynucleotides ADM01316-ADM01758 are useful in gene therapy, for developing a diagnostic marker or medicines for regulating their expression and activity, or as a target of gene therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides are useful as pharmaceutical agents. The present sequence represents a protein sequence of the invention.
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                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                translational modification; sickle cell anaemia;
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                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                       Score 82; DB 7; L
Pred. No. 1.7e-05;
); Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            irreversibly sickled cell; ISC; treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SALA-) SOUTH ALABAMA MEDICAL SCI FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB12985 standard; protein; 374 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human beta-actin protein sequence.
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                                                                                                                                                                                                                               100.08;
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                                                                                                                                                                                                                                                   100.08;
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nes 15; Conservative
                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                           1 GRPRHQGVMVGMGQK
                                                                                                                                                                                                                                                                                                                                                                            38 GRPRHOGVMVGMGOK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GRPRHQGVMVGMGQK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-498210/44.
                                                                                                                                                                                                                                              Local Similarity
es 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       post
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                                                                                                                                                                              Sequence 342 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-AUG-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US6087398-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Beta actin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Goodman SR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB12985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35
                                                                                                                                                                                                                            Query Match
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Matches
                                                                                                                                                                                                                                                        Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 9
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Expression vector contg. drug resistant marker gene - useful for transformation of thymidine kinase-deleted human cells for high levels of foreign protein prodn.
                                                                                                                                                                                                               used in the expression vector of the invention. This gene is used as the selective marker in the vector. The resulting vector may be used to transform a thymidine-kinase deleted cell allowing introduction of a foreign structural gene. The transformed cell may be used to produce
                                                                                                                                                                                               This sequence is encoded by a drug resistant structural gene which may used in the expression vector of the invention. This gene is used as th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to human cardiac actin (ACTC). Genotypic
                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New cardiac actin gene comprising histidine to arginine or glycine glutamic acid substitution, useful in the diagnosis of diseases associated with the mutation, specifically idiopathic dilated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cardiac actin; ACTC; human; gene therapy; IDC; chromosome 15q14; idiopathic dilated cardiomyopathy; mutant; mutein.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Posttranslationaly modified human cardiac actin mutant E361G.
                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 82; DB 2; Length 375; 100.0%; Pred. No. 1.9e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Wild-type Glu substituted by Gly"
                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                    Disclosure; Page 5-7; 7pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB15017 standard; protein; 375 AA.
                                                                                                                                                                                                                                                                                         large amounts of useful protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 3; Page; 36pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-00106217.
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                                                                                                                                                                                                                                                                                                                                                                                                                             1 GRPRHOGVMVGMGQK 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                          GRPRHQGVMVGMGQK 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Olson TM, Keating MT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-375488/32.
                                              WPI; 1994-094836/12
                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference 361
            (TOYM ) TOYOBO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAA73739
                                                                N-PSDB; AAQ44861
                                                                                                                                                                                                                                                                                                                         Sequence 375 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cardiomyopathy.
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Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB15017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 12
AAB15017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CXSXLTTTXXBXXBXXBXXBXXTTTTXXSXXXXXXCXXCX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  In the example, a beta-actin expression vector providing the beta-actin promoter region, a polylinker and a polyadenylation signal was constructed where the expression construct was present on a vector having a bacterial origin of replication, as well as a marker for selection in a mammalian host. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     structural gene; expression vector; selective; marker; thymidine-kinase deleted cell.
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    used for expression of

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 82; DB 1; Length 375; 100.0%; Pred. No. 1.9e-05; ive 0; Mismatches 0; Indels
                                                                                                                                                                    Actin fibre, actin film; recombinant beta-actin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Beta-actin gene and regulatory elements polypeptide(s) in mammalian host cells.
                                                                                                                                                                                                                                                                                                                                                                             (STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                             Gunning PW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example; Page 23-24; 32pp; English.
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              AAP61532 standard; protein; 375 AA
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                                                                                (revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.
Best Local Similarity 100.
Matches 15, Conservative
                                                                                                                                    Sequence of beta-actin
                                                                                                                                                                                                                                                                                                                                                                                                               Kedes LH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1986-077015/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAN60172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 375 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JP06038773-A
                                                                                                                                                                                                                                                                                                                                            13-SEP-1984;
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                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                               Leavitt JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-OCT-1994
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                                                                                25-MAR-2003
13-SEP-1991
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                                                                                                                                                                                                                                        EP174608-A.
                                                AAP61532;
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Drug

RESULT 11

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AAR50328

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(IDC). The ACTC gene maps to chromosome 15q14. Six. PCR primer pairs (AAA49020 to AAA49011) have been developed to allow analysis of the six exons of ACTC. Studies of two families with IDC showed the presence of two mutations, one in exon 5 and one in exon 6. The present sequence is mutant of posttranslationaly modified ACTC without the initial two protein may be used in a variety of methods for drug screening and for rational drug design. The ACTC gene may be used to treat IDC by gene rational drug design. The ACTC gene may be used to treat IDC by gene subjects likely to develop or who already have IDC. Note: The present sequence is not shown in the specification but is derived from the ACTC sequence described in AAY94569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is human cardiac actin (ACTC) protein, without the initial Met-Cys which is posttranslationally removed. Genotypic analyses show that ACTC is linked to idiopathic dilated cardiomyopathy (IDC). The ACTC gene maps to chromosome 15414. Six PCR primer palrs (AAA49020 to AAA49031) have been developed to allow analysis of the six exons of ACTC studies of two families with IDC showed the presence of two mutations, one in exon 5 and one in exon 6. The mutations are G to A in codon 312 (Arg312His) and A to G in codon 361 (Glu361Gly). The ACTC protein may be used in a variety of methods for drug screening and for rational drug design. The ACTC gene may be used to treat IDC by gene therapy. Analysis of the ACTC gene provides early identification of subjects likely to
analyses show that ACTC is linked to idiopathic dilated cardiomyopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or glycine to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human cardiac actin protein after posttranslational modification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New cardiac actin gene comprising histidine to arginine or glyci
glutamic acid substitution, useful in the diagnosis of diseases
associated with the mutation, specifically idiopathic dilated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 82; DB 3; Length 375;
Pred. No. 1.9e-05;
Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cardiac actin; ACTC; human; gene therapy; IDC; 15q14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY94569 standard; protein; 375 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     idiopathic dilated cardiomyopathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 3; Col 61-62; 36pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UTAH ) UNIV UTAH RES FOUND
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Best Local Similarity 100.
Matches 15, Conservative
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N-PSDB; AAA49032.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 375 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cardiomyopathy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New cardiac actin gene comprising histidine to arginine or glycine to glutamic acid substitution, useful in the diagnosis of diseases associated with the mutation, specifically idiopathic dilated
                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                            Cardiac actin; ACTC; human; gene therapy; IDC; chromosome 15q14; idiopathic dilated cardiomyopathy; mutant; mutein.
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                                                                                                                                                                                                                                                                                                                                                             Posttranslationaly modified human cardiac actin mutant R312H.
                                                                  Length 375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Wild-type Arg substituted by His"
                                                                Score 82; DB 3; I
Pred. No. 1.9e-05;
); Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                         AAB15016 standard; protein; 375 AA.
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100.0%; Pr
:ive 0;
develop or who already have IDC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 3; Page; 36pp; English.
                                                                                                                                    1 GRPRHQGVMVGMGQK 15
                                                                                                                                                                    36 GRPRHQGVMVGMGQK 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UTAH ) UNIV UTAH RES FOUND.
                                                                                                                                                                                                                                                                                                                            07-DEC-2000 (first entry)
                                                                Query Match 100.
Best Local Similarity 100.
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-375488/32.
N-PSDB; AAA73738.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference 312
                                Sequence 375 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
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100.0%; Score 82; DB 3; Length 375;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to in vitro methods for the detection of skin stress and/or skin againg in humans and animals based on the determination of spondin 2, catheppsin L, actin gamma 1 or vimentin fragments secreted by fibroblast from the skin under test. Use of the methods in a test for potential cosmetics and pharmaceuticals with an effect on these skin conditions and products containing vimentin fragments are also included. Products containing vimentin fragments are effective in the regulation, especially maintenance, of skin homeostasis
                Gaps
                                                                                                                                                                                                                                                                                 Human, dermatological, skin stress, ageing, spondin 2, cathepsin L, actin gamma 1, vimentin, fibroblast, skin, cosmetic, pharmaceutical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 82; DB 5; Length 375; 100.0%; Pred. No. 1.9e-05; ive 0; Mismatches 0; Indels
                Indels
 Pred. No. 1.9e-05; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Foerster T;
                                                                                                                                                         ABB77395 standard; protein; 375 AA.
 l Similarity 100.0%; P:
15; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                        09-OCT-2000; 2000DE-01050274.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-OCT-2000; 2000DE-01050274
                                                                36 GRPRHQGVMVGMGQK 50
                                              1 GRPRHQGVMVGMGQK 15
                                                                                                                                                                                                                     (first entry)
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Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Petersohn D, Schmitt G,
                                                                                                                                                                                                                                                   Human actin gamma 1.
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Best Local Similarity
Matches 15; Conserva
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ABB77395
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Search completed: April 8, 2005, 10:50:42 Job time : 62.4 secs

ò g Sequence 8452, A Sequence 23336, Sequence 18055, Sequence 28861,

Sequence

29187

Sequence Sequence Sequence Sequence

27806,

Sequence Sequence Sequence

Sequence Sequence S

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Run on:

Sequence:

Searched:

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OTHER INFORMATION: Description of Artificial Sequence: synthetic; OTHER INFORMATION: peptide US-08-505-250-17
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US-09-252-991A-32294
US-09-270-76-42609
US-09-398-016-6656
US-09-949-016-6656
US-09-9252-991A-23336
US-09-252-991A-28861
US-09-252-991A-28861
US-09-252-991A-28861
US-09-252-991A-29187
US-09-444-336-8
US-09-444-336-9
US-09-444-336-1
US-09-444-336-2
US-09-944-336-2
US-09-944-336-2
US-09-944-336-2
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US-09-944-336-2
US-09-949-016-8890
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Patent No. 6183983
GENERAL INFORMATION:
APPLICANT: Sato, Haruya
APPLICANT: Sato, Haruya
APPLICANT: Suzuki, Kokichi
APPLICANT: Suzuki, Kokichi
APPLICANT: Sakagami, Masahiro
APPLICANT: Sakagami, Masahiro
APPLICANT: Taniguchi, Makoto
TITLE OF INVENTION: PROTEIN MODIFICATION METHOD
FILE REFERENCE: 110-51
CURRENT APPLICATION NUMBER: US/08/505,250
CURRENT APPLICATION NUMBER: PCT/JP95/00298
EARLIER APPLICATION NUMBER: PCT/JP95/00298
EARLIER APPLICATION NUMBER: PCT/JP95/00298
EARLIER APPLICATION NUMBER: JP 198187/94
EARLIER PILING DATE: 1994-08-23
NUMBER OF SEQ ID NOS: 53
NUMBER OF SEQ ID NOS: 53
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US-08-505-250-17
Sequence 17, Application US/08505250
Patent No. 6322996
GENERAL INFORMATION:
APPLICANT: Sato, Haruya
APPLICANT: Sauch, Keiji
APPLICANT: Sazuki, Kokichi
APPLICANT: Sakagami, Masahiro
APPLICANT: Taniguchi, Makoto
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Best Local Similarity 100.0%; Pr
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ORGANISM: Artificial Sequence
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63.863 Million cell updates/sec
                                                                                                                                                                                                      April 8, 2005, 09:58:57; Search time 17.5333 Seconds
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                                   GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-949-016-11057
US-09-949-016-11313
US-09-248-796A-14109
US-09-621-976
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US-09-252-991A-32227
US-09-489-039A-10979
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-09-306-446C-2
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US-09-917-254-53
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3-08-494-151-14
3-09-106-217-16
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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82
1 GRPRHQGVMVGMGQK 15
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Maximum DB seq length: 200000000
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Perfect score:
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Best Local Similarity 100.0%; Pred. No. 4.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                              Score 82; DB 3; Length 374;
Pred. No. 4.8e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-494-151-14
) Sequence 14, Application US/08494151
patent No. 5840526
) GENERAL INFORMATION:
APPLICANT: Van Ooyen, Albert Johannes Joseph
TITLE OF INVENTION: Transformation of Phaffia rhodozyma
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPERSENT ADDRESSE:
CONTEST: 2000 Pennsylvania Ave. N.W., Suite 5500
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: FIOLOGY disk
COMPUTER: IBM PC COMPAtible
OMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OMPUTER: IBM PC COMPATIBLE
OMPATIBLE PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/494,151
FILING DATE: 23-UN-1995
CLASSIFICATION NUMBER: 29,959
REGISTRATION NUMBER: 29,959
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAK: (202) 887-0763
                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABSON-106-217-16
Sequence 16, Application US/09106217
Patent No. 60835/6
GENERAL INFORMATION:
APPLICANT: Keating, Mark T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14:
                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0%;
Matches 15; Conservative 0
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36 GRPRHQGVMVGMGQK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-494-151-14
                                                            INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
FRAGMENT TYPE:
ORIGINAL SOURCE
                                                                                                                                          CELL TYPE:
CELL LINE:
US-08-609-236-6
                                                STRAIN:
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JAPLICANT: Steven R. Goodman

TITLE OF INVENTION: No. 608739Bel Sickle Cell Anemia Treatment

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:
ADDRESSES: McGregor & Adler, LLP
STREET: 8011 Candle Lane
CITY: Houston

STREET: Fexas

COUNTRY: USA
ZIP: 77071

COMPUTER: ADDRESSER: McGregor & Adler, LLP
STREET: Boby disk
COMPUTER: ADDRESSER: McGregor & Adler, LLP
STREET: Boby disk
COMPUTER: ADDRESSER: McGregor & Adler
COMPUTER: ADDRESSER: McGregor & Macintosh
SOFTWARE: McCrosoft Word for Macintosh
CURRENT APPLICATION DATA: March 1, 1996
CLASSIFICATION NUMBER: 60/002, 288
FILING DATE: August 14, 1995
CLASSIFICATION: 514
PRIOR APPLICATION NUMBER: 60/002, 288
FILING DATE: August 14, 1995
CLASSIFICATION NUMBER: 35, 423
REGISTRATION NUMBER: 35, 423
REFERENCE/DOCKET NUMBER: D5807
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEGRAPHONE: 713-777-5908
                                                                                                                                                                                                                                                                                                                                  ) OTHER INFORMATION: Description of Artificial Sequence: synthetic J. OTHER INFORMATION: peptide US-08-505-250-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 82; DB 3; I
100.0%; Pred. No. 2.1e-07;
    TITLE OF INVENTION: PROTEIN MODIFICATION METHOD
                          FILE REFERENCE: 110-511
CURRENT APPLICATION NUMBER: US/08/505,250
CURRENT FILING DATE: 1995-11-29
PRIOR APPLICATION NUMBER: PCT/JP95/00298
PRIOR FILING DATE: 1995-02-27
PRIOR FILING DATE: 1995-02-27
PRIOR FILING DATE: 1994-08-23
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PREENTIN VET: 2.0
SERIOTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-609-236-6
; Sequence 6, Application US/08609236
; Patent No. 6087398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 GRPRHQGVMVGMGQK 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 713-777-6908
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 100.
nes 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGI. ... MOLECULE TYPE: DESCRIPTION: Protein ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Amino acid
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Matches
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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: 06/0949,016
CURRENT FILING DATE: 2000-00-10-20
PRIOR APPLICATION NUMBER: 66/231,768
PRIOR APPLICATION NUMBER: 66/237,768
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
FINDR APPLICATION NUMBER: 66/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
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                                                                                                                                                                                                                                                                   Kirk M.
DIAGNOSTIC TEST FOR DETERMINING
MALIGNANCY OF SMOOTH MUSCLE TUMORS
                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: MCHUGH, KIRK M.
TITLE OF INVENTION: DIAGNOSTIC TEST FOR DETERMININ
TITLE OF INVENTION: MALIGNANCY OF SMOOTH MUSCLE TU
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
ADDRESSEE: No. 5710003ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: -US/08/588,113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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; Sequence 6100, Application US/09949016
; Patent No. 6812339
                                                                                                                                                                            US-08-588-113-2
; Sequence 2, Application US/08588113
; Patent No. 5710003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY AGENT INFORMATION:
NAME: RAIDh, Rebecca L.
REGISTRATION NUMBER: 35,152
REFERENCE/DOCKET NUMBER: TJU-:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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                                                                                  GRPRHQGVMVGMGQK 50
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.
Matches 15; Conservative
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TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein US-08-588-113-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: PA
COUNTRY: U
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APPLICANT: Furness, Michael
APPLICANT: Buchbinder, Jenny
APPLICANT: Buchbinder, Jenny
APPLICANT: Buchbinder, Jenny
FILE REFERENCE: PA-0041 US
CURRENT APPLICATION NUMBER: US/09/976,594
CURRENT FILING DATE: 2001-10-12
PRIOR PILING DATE: 2001-10-12
PRIOR FILING DATE: 2000-10-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
APPLICANT: Olson, Timothy M.
TITLE OF INVENTION: Actin Mutations in Dilated
TITLE OF INVENTION: Cardiomyopathy, a Heritable Form of Heart Failure
NUMBER OF SEQUENCES: 18
CORRESPONDENCES: ADDRESS:
ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
STREET: 555 Thirteenth Street, N.W., Suite 701 East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 82; DB 3; Length 375; 100.0%; Pred. No. 4.8e-06;
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; OTHER INFORMATION: Incyte ID No. 6673549 1837317CD1
US-09-976-594-731
                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/106,217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2323-125
                                                                                                                                                                                                                                                                                         ZIP: 2004
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 731, Application US/09976594
Patent No. 6673549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TLASSIFICATION:
ATTORNEY/ASENT INFORMATION:
NAME: Saxe, Srephen A.
REGISTRATION NUMBER: 38,609
REFERENCE/DOCKET NUMBER: 2323
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-783-6040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
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INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GRPRHQGVMVGMGQK 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36 GRPRHOGVMVGMGQK 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 375 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15; Conservative
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SOFTWARE: PERL Program
SEQ ID NO 731
LENGTH: 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                                               STREET: Tower
CITY: Washington
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                        U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 6
US-09-976-594-731
                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-106-217-16
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FEATURE:
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                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/09106217
Patent No. 6063576
GENERAL INFORMATION:
APPLICANT: Clson, Timothy M.
TITLE OF INVENTION: Actin Mutations in Dilated
TITLE OF ENVENTION: Cardiomyopathy, a Heritable Form of Heart Failure
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSE: Rothwell, Figg, Ernst & Kurz, P.C.
STREET: S55 Thirteenth Street, N.W., Suite 701 East
                                                                                                                                                                        Gabs
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                                                                                                                                   Length 376;
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                                                                                                                               100.0%; Score 82; DB 4; Length 37 100.0%; Pred. No. 4.8e-06; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Washington
STATE: DC
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.8e-06;
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100.0%; Pred. No. 4.8e-06
tive 0; Mismatches 0
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 6100 LENGTH: 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/106,217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: SAXe, STEPDED A.
REGISTRATION NUMBER: 38,609
REFERENCE/DOCKET NUMBER: 2323
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-783-6040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 202-783-6031
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                           1 GRPRHQGVMVGMGQK 15
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amino acid
                                                                                                                               Query Match 100.
Best Local Similarity 100.
Matches 15; Conservative
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Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein US-09-106-217-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                        ) ORGANISM: Human
US-09-949-016-6100
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US-09-919-172-33
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                                                          TYPE: PRT
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Sequence 33, Application US/09919172; Patent No. 6673545; GENERAL INFORMATION: APPLICANT: Faris, Mary

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Sequence 7021, Application US/09949016
Patent No. 6812339
Facent No. 6812339
Fatent No. 6812339
Fatent No. 6812339
Fatent No. 6812339
FATEL OF INVENTION:
FAPPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: G0/241,755
FRIOR APPLICATION NUMBER: 60/241,755
FRIOR FILING DATE: 2000-10-20
FRIOR FILING DATE: 2000-10-3
FRIOR FILING DATE: 2000-10-03
FRIOR PILING DATE: 2000-10-03
FRIOR APPLICATION NUMBER: 60/231,498
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APPLICANT: Mutter, George
APPLICANT: Mutter, George
TILE REFERENCE: BOSOL/7224 (JRV)
CURRENT FILING DATE: 2001-07-27
PRIOR FILING DATE: 2001-07-27
PRIOR FILING DATE: 2001-07-28
NUMBER OF SEQ ID NOS: 102
SOFTWARE: Patentin version 3.0
SOFTWARE: Patentin version 3.0
TYPE: PRI
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                                                                                                                                                                                                                                                                                                                                          ; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673545 1709118CD1
US-09-919-172-33
APPLICANT: TURNET, Christopher M.
TITLE OF INVENTION: PROSTATE CANCER MARKERS
FILE REFERENCE: PA-0036 US.
CURRENT APPLICATION NUMBER: US/09/919,172
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/222,469
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 102
SOFTWARE: PERL PROGRAM
SEQ ID NO 33
LENGTH: 377
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; Sequence 53, Application US/09917254
; Patent No. 6703204
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Best Local Similarity 100.0
Matches 15; Conservative
                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Homo Sapiens
US-09-917-254-53
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Query Match
Best Local Similarity
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ORGANISM: Human
                         ORGANISM: Human
                           US-09-949-016-11313
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    TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FARENTAL INFORMATION:
APPLICANT' VENTER, J. Craig et al.
APPLICANT' VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION NUMBER: 00/949,016
CURRENT APPLICATION NUMBER: 00/241,755
FRIOR APPLICATION NUMBER: 60/241,755
FRIOR FILING DATE: 2000-10-03
FRIOR FILING DATE: 2000-10-03
FRIOR FILING DATE: 2000-10-03
FRIOR FILING DATE: 2000-10-03
FRIOR APPLICATION NUMBER: 60/237,768
FRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FABESEQ for Windows Version 4.0
LENGTH: 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FACELLANT: UNIVERMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: 06/241,755
PRIOR FILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FRESEQ for Windows Version 4.0
SEQ ID NO 10757
LENGTH: 402
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                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                Mismatches
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7721
LENGTH: 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 10757, Application US/09949016 Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-949-016-9424
; Sequence 9424, Application US/09949016
; Patent No. 6812339
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Best Local Similarity 100.0
Matches 15; Conservative
                                                                                                                                                                                                    Query Match 100.
Best Local Similarity 100.
Matches 15; Conservative
                                                                                                            ; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
US-09-949-016-10757
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

April 8, 2005, 10:53:18; Search time 42.6667 Seconds (without alignments) 116.718 Million cell updates/sec Run on:

US-09-423-351C-3 82 1 GRPRHQGVMVGMGQK 15

Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1418010 seqs, 331997259 residues Searched:

1418010 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published Applications AA:*

1: \cgn2 \( \) \cgn2 \( \) \( \) \cgn2 \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \ /prodata/1/pubpa/U310C_PUBCOMB.pep: /prodata/1/pubpa/U310D_PUBCOMB.pep: /prodata/1/pubpa/U310_TBW_PUB.pep:* /prodata/1/pubpa/U311_NBW_PUB.pep:* /prodata/1/pubpaa/U360_NBW_PUB.pep:* /cgn2_6/ptodata/l/pubpaa/US10_NEW_PUB.pep:* /cgn2_6/ptodata/l/pubpaa/US11_NEW_PUB.pep:* /cgn2_6/ptodata/l/pubpaa/US6_NEW_PUB.pep:* /cgn2_6/ptodata/l/pubpaa/US6_PUBCOMB.pep: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result Acore Match Length DB ID Description  No. Score Match Length DB ID  1 82 100.0 105 15 US-10-264-049-3601 Sequence 18441, 3 82 100.0 201 15 US-10-264-049-4148 Sequence 4108, Ap 4 82 100.0 204 15 US-10-264-049-4148 Sequence 4108, Ap 5 82 100.0 342 15 US-10-06-31C-36 Sequence 61, Appl 6 82 100.0 375 14 US-10-108-260A-4008 Sequence 68, Appl 9 82 100.0 375 14 US-10-31C-32-381-68 Sequence 69, Appl 10 82 100.0 375 14 US-10-31C-323-88 Sequence 89, Appl 11 82 100.0 375 15 US-10-36-31-94 Sequence 5927, Appl 12 82 100.0 375 15 US-10-36-31-94 Sequence 94, Appl 13 82 100.0 375 15 US-10-36-31-94 Sequence 94, Appl 14 US-10-26-31-94 Sequence 89, Appl 15 82 100.0 375 15 US-10-36-31-94 Sequence 94, Appl 16 82 100.0 375 15 US-10-26-31-94 Sequence 89, Appl 17 82 100.0 375 15 US-10-26-31-94 Sequence 89, Appl															
Acore Match Length DB Match 100.0 105 15 82 100.0 105 15 82 100.0 201 15 82 100.0 204 15 82 100.0 342 15 82 100.0 375 15 82 100.0 375 15 82 100.0 375 15 82 100.0 375 15 82 100.0 375 15		Description	Seguence 3601, Ap	Sequence 184471,				Sequence 4008, Ap				Sequence 5927, Ap	Sequence 94, Appl		Sequence 101, App
Acore Match Length DB Match 100.0 105 15 82 100.0 105 15 82 100.0 201 15 82 100.0 204 15 82 100.0 342 15 82 100.0 375 15 82 100.0 375 15 82 100.0 375 15 82 100.0 375 15 82 100.0 375 15		QI	US-10-264-049-3601	US-10-424-599-184471	US-10-264-049-4308	US-10-264-049-4148	US-10-002-631C-56	US-10-108-260A-4008	US-10-322-281-68	US-10-205-194-93	US-10-316-253-88	US-10-369-493-5927	US-10-205-331-94	US-10-260-708-82	US-10-341-434-101
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	æ	Query	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
Result No. 1 2 2 2 2 2 4 4 4 1 1 1 1 1 1 1 1 1 1 1		Score	82	82	82	82	82	82	82	82	82	82	82	82	82
		Result No.	н	7	٣	4	S	9	7	œ	σ	10	11	12	13

Sequence 33, Appl	Sequence 64, Appl	Sequence 4, Appli	Sequence 63, Appl	Sequence 1436, Ap	Sequence 1786, Ap	Sequence 1, Appli	Sequence 32056, A	Sequence 310, App						Sequence 282905,		Sequence 162684,				Sequence 202420,			Sequence 52, Appl		Sequence 162685,	Sequence 162686,	Seguence 222816,	Sequence 223492,	Seguence 283336,	Sequence 66124, A	Sequence 121952,
US-09-919-172-33	o	US-10-333-680-4	US-10-322-281-63	US-09-925-301-1436	US-10-369-493-1786	US-10-477-369-1	US-10-029-386-32056	US-10-092-900A-310	US-10-424-599-161246	US-10-767-701-35226	US-10-767-701-47318	US-10-424-599-280811	US-10-424-599-280810	US-10-424-599-282905	US-10-767-701-42770	US-10-424-599-162684	US-10-424-599-283333	US-10-369-493-2436	US-10-437-963-179917	US-10-437-963-202420	US-10-767-701-45677	US-10-767-701-46090	US-10-338-777-52	US-10-424-599-162009	US-10-424-599-162685	US-10-424-599-162686	-565-	US-10-424-599-223492	-59	US-10-425-114-66124	US-10-437-963-121952
6	15	Н	-	6	-	Н	Н	-	Н	Н	Н	15	Н	Н	Н	m	~	Н	~	Н	Н	ч	Н	Н	Н	Н	Н	Н	٦	-	16
377	377	37.	398	413	375	375	215	393	9	100	13	136	19.	208	23(	248	347	375	376	376	376	376	37.	37.	37.	377	37.	377	37	37	377
100.0	100.0	100.0	100.0	100.0	98.8	98.8	93.9	93.9	92.7	92.7	92.7	92.7	92.7	92.7	92.7	92.7	92.7	92.7	92.7	92.7	92.7	92.7	92.7	92.7	92.7	92.7	92.7	92.7	92.7	92.7	92.7
82	82	85	83	82	81	81	77	11	9/	97	9/	92	16	26	97	97	9/	92	9/	9/	9/	9/	9/	9/	97	92	9/	9/	92	96	16
14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	33	40	41	42	43	44	45

### ALIGNMENTS

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NAME/KEY: MISC FEATURE 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1.037 1
Sequence 3601, Application US/10264049; bublication No. US20040005579A1; bublication No. US20040005579A1; general information:

GENERAL INFORMATION:

TITLE OF INVENTION:

TITLE OF INVENTION:

FILE REFERENCE: PA133P1

CURRENT FAPLICATION NUMBER: US/10/264,049

FILE REFINENCE: PA133P1

FILE REFINENCE: 2002-10-04

PRIOR APPLICATION NUMBER: PCT/US01/18569

PRIOR PRILING DATE: 2001-06-07

PRIOR FILING DATE: 2000-06-07

PRIOR FILING DATE: 2000-06-07

SOFTWARE: PALENTIN VOICE: 3.1

LENGTH: 105
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ORGANISM: Homo sapiens
FEATURE:
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Gaps 0; Length 105; 100.0%; Score 82; DB 15; Length 10 100.0%; Pred. No. 5e-06; tive 0; Mismatches 0; Indels Query Match Best Local Similarity 100. Matches 15; Conservative

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1 GRPRHQGVMVGMGQK 15 37 GRPRHQGVMVGMGQK 51 à g

RESULT

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LOCATION: (159)
OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: MISC FEATURE
LOCATION: (174)
OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; NAME/KEX: MISC_FEATURE
; LOCATION: (180)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-264-049-4308
                OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
                                                                                                                      OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REPERENCE: PA133PI US/10/264,049
CURRENT APPLICATION NUMBER: US/10/264,049
CURRENT FILING DATE: 2002-10-04
PRIOR PELLING DATE: 2001-06-07
PRIOR PELLING DATE: 2001-06-07
PRIOR PELLING DATE: 2000-06-07
PRIOR PELLING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 4360
SOPTWARE: Patentin Ver. 3.1
SEQ ID NO 4148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 201;
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US-10-002-631C-56
Sequence 56, Application US/10002631C
Publication No. US20030157486A1
GENERAL INPOMATION:
APPLICANT: Graff, Jonathon M.
APPLICANT: Muenter, Matthew
1 TITLE OF INVENTION: METHODS TO IDENTIFY SIGNAL SEQUENCES
PILE REFERENCE: A34943 090495.0243
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Pred. No. 9.7e-06;
; Mismatches 0;
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Pred. No. 9.9e-06;
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Sequence 4148, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
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Best Local Similarity 100.0%;
Matches 15; Conservative 0
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Best Local Similarity 100.
Matches 15; Conservative
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; ORGANISM: Homo sapiens
US-10-264-049-4148
                                                                                                                                                                                                                                                                                  NAME/KEY: MISC FEATURE LOCATION: (172)
                                                                                                                                                                          NAME/KEY: MISC FEATURE LOCATION: (159)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 204
                                                                                                  LOCATION:
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Sequence 18471. Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NOS: 285684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: MISC FEATURE LOCATION: (135)
OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
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; Publication No. US2004000557941
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; TILE REFERENCE: PA1391
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR APPLICATION NUMBER: DCT/US01/18569
; PRIOR APPLICATION NUMBER: DCT/US01/18569
; PRIOR PILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: Patentin Ver. 3.1
; SEQ ID NO 4308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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US-10-424-599-184471
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Matches 15; Conservative
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OTHER INFORMATION: Xaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Glycine max
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US-10-264-049-4308
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Sequence 93, Application US/10205194

Sequence 93, Application No. US20030134301A1

Bublication No. US20030134301A1

GENERAL INFORMATION:

APPLICANT: Warner-Lambert Company

APPLICANT: Dixon, Alistair

APPLICANT: Brooksbank, Robert

APPLICANT: Pinnock, Robert

APPLICANT: Pinnock, Robert

TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain

FILE REFERENCE: WL-A-018201

CURRENT FILING DATE: 5200-07-24

PRIOR APPLICATION NUMBER: GB 0118354.0

PRIOR PILING DATE: 2010-07-27

NUMBER OF SEQ ID NOS: 177

SOFTWARE: Patentin Ver. 2.1

SEC ID NO 93

LEWAND: APPLICATION OF 93

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: The Procter & Gamble Company
APPLICANT: Peters, Kevin
APPLICANT: Thompson, Larry
APPLICANT: Thompson, Larry
APPLICANT: Thompson, Larry
APPLICANT: Thompson, Larry
APPLICANT: Greis, Kenneth
TITLE OF INVENTION: Anglogenesis Modulating Proteins
TITLE OF INVENTION: Anglogenesis Modulating Proteins
TITLE OF INVENTION: Anglogenesis Modulating Proteins
TILE REFERENCE: 8865M
CURRENT FILING DATE: 2002-12-10
PRIOR PELING DATE: 2002-02-08
NUMBER OF SEQ ID NOS: 308
SOFTWARE: Patentin version 3.1
SEQ ID NO 88
LENGTH: 375
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Cytoplasmic gamma isoform of actin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 82; DB 14;
100.0%; Pred. No. 1.8e-05;
iive 0; Mismatches 0;
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100.0%; Pred. No. 1.8e-05;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 88, Application US/10116253; Publication No. US20030162706A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36 GRPRHQGVMVGMGQK 50
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  36 GRPRHQGVMVGMGQK 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Rattus norvegicus US-10-316-253-88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100. Matches 15; Conservative
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Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Rattus
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US-10-369-493-5927
                                                                   RESULT 8
US-10-205-194-93
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US-10-316-253-88
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                                                                                                                                                                                                                                                                             Score 82; DB 14; Length 219;
Pred. No. 1.1e-05;
Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4008, Application US/10108260A; Sequence 4008, Application No. US20040005560AI; Publication No. US20040005560AI; GENERAL INFORMATION:
APPLICANT: HELLX RESEARCH INSTITUTE; TILLE OF INVENTION: No. US20040005560AIel full length cDNA; FILE REFERENCE: HI-A0106; CURRENT APPLICATION NUMBER: US/10/108,260A; CURRENT FILING DATE: 2002-03-27; NUMBER OF SEQ ID NOS: 5458; SOFTWARR: Patentin Ver. 2.1; SEQ ID NO 4008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 342;
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Publication No. US20040126762A1
GENERAL INFORMATION:
APPLICANT: David W. Morris
APPLICANT: Marc S. Malandro
TITLE OF INVENTION: Novel Compositions and Methods in Cancer FILE REFERENCE: 529452001000
CURRENT APPLICATION NUMBER: US/10/322,281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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100.0%; Pred. No. 1.7e-05;
iive 0; Mismatches 0;
                CURRENT FILING DATE: 2001-10-31
PRIOR APPLICATION NUMBER: 60/300,309
PRIOR FILING DATE: 2001-06-21
PRIOR FILING DATE: 2001-06-21
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 56
LENGTH: 219
TYPE: PRT
ORGANISM: Homo sapiens
CURRENT APPLICATION NUMBER: US/10/002,631C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 866
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 68
LENGTH: 371
TYPE: PRT
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Best Local Similarity 100.0%;

Matches 15; Conservative 0,
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Best Local Similarity 100.0
Matches 15; Conservative
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US-10-108-260A-4008
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APPLICANT: Origone Technologies
TITLE OF INVENTION: Differentially Regulated Prostate Cancer Genes
FILE REFERENCE: 9U 204 205 R1
CURRENT APPLICATION NUMBER: US/10/341,434
CURRENT FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: US 60/348,119
PRIOR FILING DATE: 2002-01-15
PRIOR FILING DATE: 2002-01-15
NUMBER OF SEQ ID NOS: 238
SOFTWARE: Patentin version 3.1
SEQ ID NO 101
                                                                                                                                                                                                                                                                                                   Length 375;
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APPLICANT: Old, Lloyd
TITLE OF INVENTION: Human Sarcoma-Associated Antigens
FILE REFERENCE: L00461/70138
CURRENT APPLICATION NUMBER: US/10/260,708
CURRENT FILING DATE: 2002-09-30
NUMBER OF SEQ ID NOS: 96
SOFTWARE: PatentIn version 3.1
SEQ ID NO 82
LENGTH: 375
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100.0%; Pred. No. 1.8e-05;
tive 0; Mismatches 0;
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100.0%; Pred. No. 1.8e-05;
tive 0; Mismatches 0;
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APPLICANT: Furner, Christopher M.
APPLICANT: Turner, Christopher M.
TITLE OF INVENTION: PROSTATE CANCER MARKERS
FILE REFERENCE: PA-0036 US
CURRENT APPLICATION NUMBER: US/09/919,172
CURRENT APPLICATION NUMBER: 60/222,469
PRIOR APPLICATION NUMBER: 60/222,469
PRIOR APPLICATION NUMBER: 60/222,469
NUMBER OF SEQ ID NOS: 102
SOFTWARE: PERL Program
SEQ ID NO 33
LENOTH: 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 101, Application US/10341434; Publication No. US20030215835A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 33, Application US/09919172; Patent No. US20020119463A1; GENERAL INFORMATION:
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Best Local Similarity 100.0
Matches 15; Conservative
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; ORGANISM: Homo sapiens
US-10-341-434-101
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ORGANISM: Homo sapiens
FEATURE:
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US-10-260-708-82
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Best Local Similarity
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                                                          APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
FILE REFERENCE: 38-10 (52.05.2)
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 5927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Warner-Lambert Company
APPLICANT: Lee, Kevin
APPLICANT: Lee, Kevin
APPLICANT: Brooksbank, Robert
APPLICANT: Brooksbank, Robert
APPLICANT: Pinnock, Robert
APPLICANT: Pinnock, Robert
TITLE OF INVENTION: Lednification and Use of Molecules Implicated in Pain
FILE OF INVENTION: USABLES
CURRENT FLING DATE: 2002-07-24
FILE REPERENCE: WL-A-018199
CURRENT APPLICATION NUMBER: US 0118354.0
FRIOR FILING DATE: 2001-07-27
NUMBER OF SEQ ID NOS: 117
SEQ ID NO 94
LENGTH: 375
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    Sequence 5927, Application US/10369493
Publication No. US20030233675A1
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Publication No. US20040063101A1
GENERAL INFORMATION:
APPLICANT: Scanlan, Matthew
APPLICANT: Lee, Sang-Yull
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 94, Application US/10205331
Publication No. US20040058326A1
                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-5927
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US-10-205-331-94
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US-10-260-708-82
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Best Local Similarity 100.0%; Score 82; DB 15; Length 377;
Best Local Similarity 100.0%; Pred. No. 1.9e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0
                                         Query Match
100.0%; Score 82; DB 9; Length 377;
Best Local Similarity 100.0%; Pred. No. 1.9e-05;
Matches 15; Conservative 0; Mismatches 0; Indels
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020119463A1 1709118CD1
US-09-919-172-33
                                                                                                                                                        TYPE: PRT
CORGANISM: Homo sapiens
US-10-236-031B-64
                                                                                                                                          RESULT 15
US-10-236-031B-64
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Search completed: April 8, 2005, 12:50:57 Job time : 42.6667 secs

1 GRPRHQGVMVGMGQK 15 |||||||||||||| 38 GRPRHQGVMVGMGQK 52

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GenCore version 5.1.6
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OM protein - protein search, using sw model

April 8, 2005, 09:58:56; Search time 9.33333 Seconds Run on:

(without alignments)
154.634 Million cell updates/sec

US-09-423-351C-3 82 1 GRPRHQGVMVGMGQK 15 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

*:6/ Database :

pir1:* pir2:* pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

	Description	beta,	actin 5C - fruit f		actin CA15 - sea s	actin 3 - fruit fl	beta -	, fetal	type 5,		+	ď	_		actin beta - rat	beta, c	beta -	beta - h	actin gamma 1 - hu			actin beta, non-mu		_	beta-		actin beta, cytoso	actin beta - goose	alpha,	actin - Phaffia rh	
SUMMAKIES	ID	C43616	A28258	I49465	A61043	A03000	S05430	B25819	A26559	ATBOB	ATBOG	JC5818	ATBOSM	ATRB	ATRTC	A48324	ATCHB	ATHUB	ATHUG	ATMSB	ATMSG	ATRBB	S11222	T25272	871125	S71124	871126	A55001	A54728	S70377	
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de	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	
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actin 7 - fruit fl	actin gamma, cytos	actin gamma, smoot	actin 8 - fruit fl	actin CyI - sea ur	Actin-1A - nematod	actin 87E - fruit	actin - fruit fly	actin, cytosolic -	actin, muscle - st	actin 15A - sea ur	actin - sea urchin	actin gamma, enter	actin - Hydra atte	actin (clone gen3)	actin (clones Ia a	
ATFF7	A43552	ATCHSM	ATFF8	ATURS	A48449	S04538	JC1246	JS0189	JS0190	807288	809578	A40261	JQ0154	JN0832	JN0833	
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100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	
82	82	82	82	82	82	82	82	82	82	82	82	82	82	82	82	
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

## ALIGNMENTS

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catin beta, cytosolic - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Species: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 09-Jul-2004
C;Accession: C43616
R;Paterson, B.M.; Eldridge, J.D.
Science 224, 1436-1438, 1984
A;Fittle: alpha-Cardiac actin is the major sarcomeric isoform expressed in embryonic avia A;Reference number: A43616; MUID:84223949; PMID:6729461
A;Reference number: A43616; MUID:84223949; PMID:6729461
A;Recession: C43616
A;Recession: C43616
A;Residues: 1-86 c-PAT>
A;Residues: 1-86 c-PAT>
A;Cross-references: UNIPROT:Q90736; GB:K02173; NID:g211054; PIDN:AAA98513.1; PID:g211055
C;Superfamily: actin
C;Reywords: cytosol; methylated amino acid
F;73/Modified site: 3'-methylhistidine (His) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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100.0%; Score 82; DB 2; Length 86
Best Local Similarity 100.0%; Pred. No. 7e-07;
Matches 15; Conservative 0; Mismatches 0; Indels
RESULT 1
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# 1 GRPRHQGVMVGMGQK 15

36 GRPRHQGVMVGMGQK 50 à 셤

# RESULT 2 A28258

actin 5C - fruit fly (Drosophila melanogaster)

C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004
R;Vigoreaux, J. 1161-1171, 1987
A;Title: Stage-specific selection of alternative transcriptional initiation sites from the A;Title: Stage-specific selection of alternative transcriptional initiation sites from the A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: manna
A;Molecule type: manna
C;Genetics:

A;Gene: FlyBase:Act5C A;Cross-references: FlyBase:FBgn0000042 C;Superfamily: actin C;Keywords: methylated amino acid F;74/Modified site: 3'-methylhistidine (His) #status predicted

100.0%; Score 82; DB 2; Length 137; 100.0%; Pred. No. 1.1e-06; Query Match Best Local Similarity

à 셤

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A;Molecule type: DNA
A;Residues: 1-308 <FYRS-
$\forestyle{\text{Cross-references}}$. UNIPPOT:P02572
A;Note: there are 68 unsequenced residues between positions 160 and 161. Partial sequenc
A;Note: the authors translated the codon GTT for residue 263 as 11e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Riliu, Z.; Zhu, Z.; Roberg, K.; Faras, A.J.; Guise, K.S.; Kapuscinski, A.R.; Hackett, P. Nucleic Acids Res. 17, 5850, 1989
A;Title: The beta-actin gene of carp (Ctenopharyngodon idella).
A;Reference number: S05430, MUID:89345185; PMID:2762162
A;Accession: S05430
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C;Species: Mus musculus (house mouse)
C;Date: 23-Aug-1987 #sequence_revision 23-Aug-1987 #text_change 09-Jul-2004
C;Accession: B25819
R;Alonso, S.; Minty, A.; Bourlet, Y.; Buckingham, M.
R;Alonso, S.; Minty, A.; Bourlet, Y.; Buckingham, M.
A;Alonso, S.; Minty, A.; Bourlet, Y.; Buckingham, M.
A;Title: Comparison of three actin-coding sequences in the mouse; evolutionary relations
A;Reference number: A25819; MUID:86200234; PMID:3084797
                                                                                     C;Accession: A03000
R;Fyrberg, E.A.; Bond, B.J.; Hershey, N.D.; Mixter, K.S.; Davidson, N.
Call 24, 107-116, 1981
A;Title: The actin genes of Drosophila: protein coding regions are highly conserved but A;Reference number: A03000; MUID:81210174; PMID:6263481
A;Accession: A03000
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ctin 3 - fruit fly (Drosophila melanogaster) (fragments)
;Species: Drosophila melanogaster
;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Ctenopharyngodon idella (grass carp)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004
C;Accession: S05430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C,Superfamily: actin
C,Keywords: methylated amino acid
F;74/Modified site: 3'-methylhistidine (His) #status predicted
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Pred. No. 2.7e-06;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: FlyBase:Act42A
A;Cross-references: FlyBase:FBgn0000043
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illarity 100.0%;
Conservative 0
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Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 15; Conserv
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A;Residues: 1-328 <LIU>
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C;Species: Styela clava
S;Seach, R.L.; Jeffery, W.R.
Dev. Genet. 11, 2-14, 1990
A;Title: Temporal and spatial expression of a cytoskeletal actin gene in the ascidian St
A;Reference number: A61043; MUID:90298580; PMID:2361333
A;Reference number: A61043
A;Residues: 1-213 cBBA>
A;Rosidues: 1-213 cBBA>
A;Cross-references: UNIPROT:Q7M3Y7
C;Comment: This sequence is expressed in cells undergoing rapid cell division.
C;Superfamily: actin
C;Superfamily: actin
C;Keywords: cytoskeleton; methylated amino acid; mitosis; structural protein
F;73/Modified site: 3'-methylhistidine (His) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ,Residues: 1.158 - RES>
;Cross-references: UNIPROT:Q61273; GB:M26775; NID:g191646; PIDN:AAA37165.1; PID:g553858
;Accession: 149466
                                                                                                                                                                                                                                                           alpha-cardiac actin - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: 149465; 149466
R;Garner, I.; Multry, A.J.; Alonso, S.; Barton, P.J.R.; Buckingham, M.E.
EMBO J. 5, 2559-2567, 1986
A;Title: A 5' duplication of the alpha-cardiac actin gene in BALB/c mice is associated wherence number: 149465; MUID:87053822; PMID:3023046
A;Accession: 149465
A;Accession: 149465
A;Molecule type: DNA
A;Molecule type: DNA
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A; Modecule type: DNA
A; Residues: 1-158 (RES>
A; Cross-references: UNIPROT:Q61273; GB:M26775; NID:g191646; PIDN:AAA37165
A; Accession: 149466
A; Status: translated from GB/EMBL/DDBJ
A; Modecule type: DNA
A; Residues: 8-158 (REZ>
A; Cross-references: GB:M26776; NID:g191649; PIDN:AAA37166.1; PID:g553859
A; Cross-references: GB:M26776; NID:g191649; PIDN:AAA37166.1; PID:g553859
C; Genetics:
A; Introns: 50/3
C; Superfamily: actin
C; Keywords: cardiac muscle; heart
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Pred. No. 1.3e-06;
   Mismatches
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                                                                                                              37 GRPRHQGVMVGMGQK
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Matches 15; Conservative
   15; Conservative
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Matches 15; Conserv
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ઠે ద A; Molecule type: mRNA

RESULT S

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actin, aortic smooth muscle - bovine
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A;Residues: 1-374 <VAN>
A;Cross-references: UNIPROT:P02571
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A;Residues: 1-374 <HAU>
A;Cross-references: UNIPROT:P02571
                              GRPRHOGVMVGMGQK 15
                                                                    35 GRPRHQGVMVGMGQK 49
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Best Local Similarity 100.
Matches 15; Conservative
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Matches
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C;Species: Bos primigenius taurus (cattle)

C;Accession: E14185; A39105; A02999; A14185

R;Vandekerckhove, J; Weber, K.

Bur. J. Biochem. 90, 451-462, 1978

A;Title: Actin amino-acid sequences. Comparison of actins from calf thymus, bovine brain

A;Reference number: A14185; MUID:79045349; PMID:213279

A;Residues: L-374 «VAM»

A;Reference number: A39105; MUID:84032385; PMID:6195151

A;Reference number: A39105

A;Reference number: A39105

A;Residues: 76-227;344-374 «DEG>
A;Residues: Polocked amino end; cell motility; cytoskeleton; methylated amino acid; micr
C;Superfamily: actin
C;Meywords amino end; cell motility; cytoskeleton; methylated amino acid; micr
F;1/Modified site: blocked amino end; elly #Status predicted
F;12/Modified site: blocked amino end; elly #Status predicted
                    A.Cross-references: UNIPROT:Q61275; GB:X03767; GB:J00381; GB:M10652; NID:g49869; PIDN:CAC; Superfamily: actin
C;Superfamily: actin
C;Keywords: cardiac muscle; heart; methylated amino acid; muscle; skeletal muscle
F;47/Modified site: 3'-methylhistidine (His) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  actin type 5, cytosolic - chicken
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Species: Asep-1987 #sequence_revision 09-Sep-1987 #text_change 05-Dec-1997
C;Accession: A.5. Chang, K.S.; Schwartz, R.J.
Mol. Cell. Biol. 5, 1151-1162, 1985
A;Reference number: A.26559; MUID:85213487; PMID:4000121
A;Reference number: A.26559
A;Molecule type: DNA
A;Residues: 1-362 - SER>
C;Superidamily: actin
C;Reywords: Cytosol; methylated amino acid
F;74/Modified site: 3'-methylhistidine (His) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                             Length 349;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 362;
                                                                                                                                                                                                                                                           0; Indels
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100.0%; Score 82; DB 2; L
Best Local Similarity 100.0%; Pred. No. 2.8e-06;
Matches 15; Conservative 0; Mismatches 0;
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Pred. No. 3e-06;
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100.0%;
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Best Local Similarity 100.
Matches 15; Conservative
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A; Residues: 1-349 <ALO>
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R; Vandekerckhove, J.; Weber, K.
Eur. J. Biochem. 90, 451-462, 1978
Eur. J. Biochem. 90, 451-462, 1978
A;Title: Actin amino-acid sequences. Comparison of actins from calf thymus, bovine brain A;Reference number: A14185; WUID:79045349; PMID:213279
A;Accession: B14185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Note: only peptides that differed in composition from the corresponding peptides of ra C;Comment: Vertebrate nonmuscle cells contain two highly conserved cytoskeletal actins, C;Superfamily: actin C;Keywords: blocked amino end; cell motility; cytoskeleton; methylated amino acid; micrc F;1/Modified site: blocked amino end (Glu) (probably acetylated) #status experimental F;72/Modified site: 3'-methylhistidine (His) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gamma-actin - human
C;Species: Homo sapiens (man)
C;Date: 20-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 09-Jul-2004
C;Dacession: JG5818; PC4501
R;Hauschildt, S.; Schwarz, C.; Heine, H.; Ulmer, A.J.; Flad, H.D.; Rietschel, E.T.; Jens
Biochem. Biophys. Res. Commun. 241, 670-674, 1997
A;Title: Actin: A target of lipopolysaccharid-induced phosphorylation in human monocytes
A;Reference number: JG5818; MUID:98096379; PMID:9434766
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A;Residues: 1-61;84-112;147-190;196-209;215-253;335-358 <HA2>
A;Residues: 1-61;84-112;147-190;196-209;215-253;335-358 <HA2>
C;Comment: This protein is involved in a signal transduction that eventually leads to mo C;Superfamily: actin
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C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 06-Sep-1996
C;Accession: A02997; S13480
actin gamma - bovine (tentative sequence)
C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: B14185; A02999
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100.0%; Pred. No. 3.1e-06;
iive 0; Mismatches 0;
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0; Mismatches
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       A;Residues: 48-54;68-72;235-243 <STR>A;Experimental source: skeletal muscle R;Bertrand, R; Derancourt, J.; Kassab, FEBS Lett. 345; 113-119, 1994
                                                                                                                                                                                                                                                                                                                           A; Experimental source: skeletal muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GRPRHQGVMVGMGQK 15
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Best Local Similarity 100.0
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Matches 15; Conservative
                                                                                                                                                                                                                                                          A; Molecule type: protein A; Residues: 48-64 < BER>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Accession: A38571
A;Molecule type: DNA
A;Residues: 1-375 <NUD>
                                                                                                                                                                                                                                                                                                                                                               C;Superfamily: actin
                                                                                                                                                                                                                         A; Accession: S44393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                actin beta - rat
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Nilternate names: Faction
Cippecies: Oryctolagus cuniculus (domestic rabbit)
Cippecies: Oryctolagus cuniculus
Cippecies: Oryctolagus cuniculus
Cippecies: Oryctolagus cuniculus
Cippecies: Oryctolagus cuniculus
Cippecies: Oryctolagus
Airles: The primary structure of actin from rabbit skeletal muscle. Completion and analyseference number: A92182; MUD: 75211334; PMID: 1150655
A; Mitle: The primary parterial
A; Residues: 1-2, Th. 4, Di. 6-11, 'D', 11-73, 'W', 74-78,80-234,236-308, 'T', 310-375 <COL>
A; Residues: 1-2, Th. 4, Di. 6-11, 'D', 11-73, 'W', 74-78,80-234,236-308, 'T', 310-375 <COL>
A; Roce: this sequence has been revised in references A14185 and A90406
R; Andekerchore, Ji, wheber, 'R.
Biochem: A14185, WUD: 79045349; PMID: 213279
A; Rocession: 118,69-84 < VAN>
A; Rocession: A14185, WUD: 79045349; PMID: 213279
A; Rocession: 118,69-84 < VAN>
A; Rocession: 118,69-84 < VAN>
A; Rocession: A14185, WUD: 79045349; PMID: 588555
A; Mitle: Partial amino acid sequence of brain actin and its homology with muscle actin. A; Rocesmenter: A for ferrore number: A90406; WUD: 78060866; PMID: 588555
A; Note: residue 235 has been added and residue 309 has been revised
R; Wandat, A. Miller: (') PMIJIPS MUD: 7781788
A; Rocession: SSS973; WUD: 9520993; PMID: 7781788
A; Rocession: SSS973; WUD: 9520993; PMID: 7781788
A; Rocession: Biochem
A; Residues: SSS973; WUD: 9520993; PMID: 240 to Mg2+, bound at the high-affinit A; Rocession: S70610; WUD: 970610; WUD: 97061013; A; Hiller: A; Rocession: S70610; WUD: 970610; WUD: 97061013; PMID: 9706113; A; Hiller: PMID: 970610; A; Hiller: PMID: 970610; A; Hiller: PMID: 970610; A; Hiller: PMID: 9706113; A; Hiller: PMID: 970610; A; Hiller: PMID: 970610; A; Hille
R; Vandekerckhove, J.; Weber, K.

Differentiation 14, 123-133, 1979
A; Title: The complete amino acid sequence of actins from bovine aorta, bovine heart, bov tiation.

A; Reference number: A02997; MUID:80047657; PMID:499690
A; Rolecule type: protein
A; Molecule type: protein
A; Residues: 1-375 < VAN>
R; Zevgolis, V.G.; Soliroudis, T.G.; Evangelopoulos, A.E.
Biochim. Biophys. Acta 1091, 222-230, 1991
A; Title: Phosphorylase kinase from bovine stomach smooth muscle: a Ca(2+)-dependent prot A; Recence number: $13480; MUID:91137633; PMID:1995080
A; Recence number: $13480; MUID:91137633; PMID:1995080
A; Residues: 40-49 < ZEV>
A; Reperimental source: stomach
A; Roceidues: 40-49 < ZEV>
A; Reperimental source: stomach
A; Note: this material appears to be actin of aortic smooth muscle type or a related mole C; Superfamily: actin
C; Superfamily: actin
C; Superfamily: actin
C; Keywords: acetylated amino end; methylated amino acid; muscle contraction
F; 1/Modified site: acetylated amino end (Glu) #status predicted
F; 1/3/Modified site: 3'-methylhistidine (His) #status experimental
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; Pred. No. 3.1e-06;
0; Mismatches 0;
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Best Local Similarity 100.
Matches 15; Conservative
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C;Keywords: acetylated amino end; ATP binding; methylated amino acid; muscle contraction E;1.375/Product: actin #status experimental <MAT>
F;1.375/Product: actin #status experimental <MAT>
F;1/Modified site: acetylated amino end (Asp) #status experimental
F;73/Modified site: 3'-methylhistidine (His) #status experimental
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A;Residues: 1-375 <LIU>
A;Cross.references: UNIPROT:P83750; GB:M24113; NID:g213041; PIDN:AAA68886.1; PID:g213042
A;Note: the authors translated the codon TTC for residue 21 as Pro, AAG for residue 50 a
7 as Pro
A;Note: the authors failed to translated the codon GGT for residue 42 as Gly
    m
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C;Comment: Vertebrate nonmuscle cells contain two highly conserved cytoskeletal actins,
A,Title: The covalent maleimidobenzoyl-actin-myosin head complex. Cross-linking of the A,Reference number: S44393; MUID:94259162; PMID:8200441
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R;Liu, Z.; Zhu, Z.; Roberg, K.; Faras, A.; Guise, K.; Kapuscinski, A.R.; Hackett, P.B.
DNA Seq. 1, 125-136, 1990
A;Title: Isolation and characterization of beta-actin gene of carp (Cyprinus carpio).
A;Reference number: A48324; MUID:92190540; PMID:2134183
A;Accession: A48324
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C;Date: 13-Jun-1983 #sequence_revision 13-Jun-1983 #text_change 22-Jun-1999
C;Accession: A38571; A0299
R;Nudel, U; Zakut, R.; Shani, M.; Neuman, S.; Levy, Z.; Yaffe, D.
Nucleic Acids Res. 11, 1759-1771, 1983
A;Title: The nucleotide sequence of the rat cytoplasmic beta-actin gene.
A;Reference number: A38571; MUID:83168920; PMID:6300777
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C;Species: Cyprinus carpio (common carp)
C;Date: 03-Feb-1994 #sequence_revision 11-Apr-1997 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 82; DB 1; Length 375; 100.0%; Pred. No. 3.1e-06;
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C;Comment: Vertebrate nonmuscle cells contain two highly conserved cytoskeletal actins, C;Genetics:
A;Introns 41/3; 121/3; 268/3; 328/3
A;Introns 41/3; 121/3; 268/3; 328/3
C;Superfamily: actin
C;Keywords: acetylated amino end; cell motility; cytoskeleton; methylated amino acid; mi P;2,775 product: actin beta, cytoskeletul #status predicted <AMIT:
F;2/Modified site: acetylated amino end (App) (in mature form) #status predicted
F;73/Modified site: 3'-methylhistidine (His) #status predicted
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100.0%; Score 82; DB 1; Length 375;
Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels
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Search completed: April 8, 2005, 10:53:05 Job time : 10.3333 secs

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bombyx mori
schmidtea p
schmidtea p
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oryctolagus
bos taurus
gallus gall
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score greater than or equal to the score of the result being printed,
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Eukaryota, Metazoa, Platyhelminthes, Turbellaria, Seriata, Tricladida,
Paludicola, Dugesiidae, Schmidtea.
NCBI TaxID=50054,
                                                                                            Schmidtea polychroa.
Bukaryota, Metazoa, Platyhelminthes, Turbellaria, Seriata, Tricladida,
Paludicola, Dugesiidae, Schmidtea.
NCBI_TaxID=50054;
                                                                                                                                                                                                                                       MEDIJERS 99.86847; PubMed-9518500; DOI=10.1093/nar/26.8.2031;
Pagotti A., Gabbiani G., Pascolini R., Neuville P.;
Pagotti A., Gabbiani G., Pascolini R., Neuville P.;
Pultiple isoform recovery (MRN - PCR: a simple method for the isolation of related mRNA isoforms.",
Nucleic Acids Res. 26:2031-2033(1998).
-!-FUNCTION: Actins are highly conserved proteins that are involved in various types of cell motility and are ubiquitously expressed in all eukaryotic cells (By similarity).
-!-SIMILARITY: Belongs to the actin family.
HSSP; PO2577; INM1.
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Fagotti A., Gabbiani G., Pascolini R., Neuville P.;
"Multiple isoform recovery (MIR)-PCR: a simple method for the
isolation of related mRNA isoforms.";
Nucleic Acids Res. 26:2011-2033(1998).
-!-FUNCTION: Actins are highly conserved proteins that are involved
in various types of cell motility and are ubiquitously expressed
in all eukaryotic cells (By similarity).
-!-SIMILARITY: Belongs to the actin family.

EMBL. AR027163; AAC38983.1; -.
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GO; GO:0003774; F:motor activity; IEA.
GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
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GO; GO: 0003774; E:actin filament; IEA.
GO; GO: 0005200; F:structural constituent of cytoskeleton; IEA.
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InterPro; IPR004001; Actin.
PF00022; Actin; 1.
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100.0%; Pred. No. 4.1e-06;
tive 0; Mismatches 0;
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InterPro; IPR004000; Actin_like
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PROSITE; PS00406; ACTINS_1; 1.
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Bukaryota, Metazoa, Platyhelminthes, Turbellaria, Seriata, Tricladida,
Paludicola, Dugesiidae, Schmidtea.
NCBI_TaxID=50054;
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-!-FUNCTION: Actins are highly conserved proteins that are involved in various types of cell motility and are ubiquitously expressed in all eukaryotic cells (By similarity).
-!-SIMILARITY: Belongs to the actin family.

EMBL: ARO27161; AAC38981.1; -.
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GO; GO:0005884; C:actin filament; IEA.
GO; GO:0003774; F:motor activity; IEA.
GO; GO:0003709; F:motor activity; IEA.
GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
InterPro; IPR004000; Actin_like.
submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AB186491; BAD35130.1; -.
DR InterPro; IPR004000; Actin_like.
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Best Local Similarity luv...
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Best Local Similarity 100.
Matches 15; Conservative
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RESULT 3
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RESULT 4 061376 ID 06137 AC 06137 DT 01-A1 DT 01-A1 DE ACTI

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Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
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-!- FUNCTION: Actins are highly conserved proteins that are involved in various types of cell motility and are ubiquitously expressed in all eukaryotic cells (By similarity).
-!- SIMILARITY: Belongs to the actin family.
EMBL; KO2173; AAA98513.1; -.
PIR; C43616; C43616.
                                                                                                                                         -I- FUNCTION: Actins are highly conserved proteins that are involved in various types of cell motility and are ubiquitously expressed in all eukaryotic cells (By similarity).
-I- SIMILARITY: Belongs to the actin family.
EMBL; AF191490; AAF05984.1; --
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Paterson B.M., Eldridge J.D.;
"alpha-Cardiac actin is the major sarcomeric isoform expressed in
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GO: GO:0005884; C:actin filament; IEA.
GO: GO:00053774; F:mctor activity; IEA.
GO: GO:0005200; F:structural constituent of cytoskeleton; IEA.
                                                                                                                                                                                                                                                                                                                                  GO; GO:0005884; C:actin filament; IEA.
GO; GO:0003774; F:motor activity; IEA.
GO; GO:0005200; F:atructural constituent of cytoskeleton; IEA.
InterPro; IPR004000; Actin.
InterPro; IPR004000; Actin.like.
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Pred. No. 4.2e-06;
; Mismatches 0; Indels
                                                                                         John S.J., Bilodeau-Goeseels S.;
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86 AA; 9351 MW; A55285196A328E6E CRC64;
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PROSITE; PS00406; ACTINS_1; 1.
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(TrEMBLrel. 01, I
(TrEMBLrel. 24, I
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Best Local Similarity 100.
Matches 15; Conservative
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PRINTS; PR00190; ACTIN.
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les 15; Conservative
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NON_TER 80
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                                                               SEQUENCE FROM N.A.
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NCBI_TaxID=9913;
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01-NOV-1996
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Am. J. Physiol. Cell Physiol. 283:C1646-C1654(2002).
-!- FUNCTION: Actins are highly conserved proteins that are involved in various types of cell motility and are ubiquitously expressed in all eukaryotic cells (By similarity).
-!- SIMILARITY: Belongs to the actin family.
EMBL; AF44278; AAL01885.1; --
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 24, Last annotation update)
Beta actin (Fragment).
Beta actins (Bovine).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Cetartiodactyla; Ruminantia; Bocora; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Beta-actin (Fragment).
Oryctolagus cuniculus (Rabbit).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
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GO; GO:0003774; F:motor activity; IEA.
GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=22306422; PubMed=12388084;
Wang D.-A., Du H., Jaggar J.H., Brindley D.N., Tigyi G.J.,
Watsky M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 79;
                                                                                            Score 82; DB 2; Lengtn ,...
Pred. No. 4.1e-06;
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                                   78 78 78 79 78 AA; B9DFF1108E4ADB0E CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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100.0%; Pred. No. *...
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InterPro; IPR004000; Actin_like
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PROSITE; PS00406; ACTINS_1; 1.
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Best Local Similarity
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SEQUENCE
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RESULT 6
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RESULT 7 Q9TTW4

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CYTRATN=15010-0951.0;

KMEDLINE=22480340; PubMed=12574518; DOI=10.1073/pnas.0336368100;

KMEDLINE=22480340; PubMed=12574518; DOI=10.1073/pnas.0336368100;

Mitkopp P.J., Williams B.L., Selegue J.E., Carroll S.B.;

Throsophila pigmentation evolution: divergent genotypes underlying convergent phenotypes.";

Proc. Natl. Acad. Sci. U.S.A. 100:1808-1813(2003).

Throsophila pigmentation evolution: divergent genotypes underlying convergent phenotypes.";

In Proc. Natl. Acad. Sci. U.S.A. 100:1808-1813(2003).

In various types of cell motility and are ubiquitously expressed in various types of cell motility and are ubiquitously expressed in various types of the actin family.

EMBL; AX165516; AAP12711.1; --

R HSSP; PO2568; LLCU.

R PlyBase; PBGN0066281; Dame\ActE2.
-!- FUNCTION: Actins are highly conserved proteins that are involved in various types of cell motility and are ubiquitously expressed in various types of cells (By similarity).

-! SIMILARITY: Belongs to the actin family.

REMBL; AR165541; AAP21565.1; -.

R PiyBase; PBQD066214; Dnov\ActE2.

R GO; GO:0005804; C:actin filament; IEA.

GO; GO:0005804; F:seructural constituent of cytoskeleton; IEA.

R GO; GO:0005207, R:seructural constituent of cytoskeleton; IEA.

R InterPro; IPR004001; Actin.

R Dfm; PF00022; Actin.

R Pfm; PF00022; Actin.

R Pfm; PF00022; Actin.

R Pfm; PF00022; Actin.

R Pfm; PF00022; Actin.
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GO; GO:0003774; F:motor activity; IEA.
GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila americana (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 82; DB 2; Length 96;
; Pred. No. 5e-06;
0; Mismatches 0; Indels
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01-UUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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InterPro, IPR004000; Actin_like.
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PRINTS; PR00190; ACTIN.
PROSTTE; PS00406; ACTIN.
Structural protein. 96
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PROSITE; PS00406; ACTINS_1; 1.
Structural protein.
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Matches 15; Conservative
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Best Local Similarity
Matches 15; Conserv
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Q86FV7
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Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Actins are highly conserved proteins that are involved in various types of cell motility and are ubiquitously expressed in all eukaryotic cells (By similarity).
-!- SIMILARITY: Belongs to the actin family.
EMBL; AX262761; AAP31127.1; -.
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MEDLINE=22480340; PubMed=12574518; DOI=10.1073/pnas.0336368100;
Wittkopp P.J., Williams B.L., Selegue J.E., Carroll S.B.;
"Drosophila pigmentation evolution: divergent genotypes underlying
                                                                                                                                                                                                                                                                                                                                                                                                                                Salvelinus alpinus (Arctic char).
Eukaryota, Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi;
Entinopterygii, Neopterygii; Teleostei; Euteleostei;
Procacanthopterygii; Salmoniformes; Salmonidae; Salvelinus.
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GO; GO:0005884; C:actin filament; IEA.
GO; GO:0003774; F:motor activity; IEA.
GO; GO:0005700; F:tructural constituent of cytoskeleton; IEA.
InterPro; IPR004001; Actin.
InterPro; IPR004000; Actin.like.
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Bukaryota, Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=47314;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                      (TrEMBLrel. 24, Created)
(TrEMBLrel. 24, Last sequence update)
(TrEMBLrel. 26, Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 100:1808-1813(2003).
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Pred. No. 4.7e-06;
; Mismatches 0;
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01-MAR-2004 (TrEMBLre
Beta-actin (Fragment)
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllidae; Gryllinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Adrenal gland;
Buelow H.E., Bernhardt R.;
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Actions are highly conserved proteins that are involved in various types of cell motility and are ubiquitously expressed in all eukaryotic cells (By similarity).
-!- SIMILARITY: Belongs to the actin family.
HSSP; P02577; INMI.
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Dev. Growth Differ. 0:0-012002).

-!-FUNCTION: Actins are highly conserved proteins that are involved in various types of cell motility and are ubiquitously expressed in all eukaryotic cells (By similarity).
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Cytoplasmic actin (Fragment).
Cytoplasmic actin (Fragment).
Evit porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
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GO; GO:0005884; C:actin filament; IEA.

GO; GO:0003774; F:motor activity; IEA.

GO; GO:000500; F:structural constituent of cytoskeleton; IEA.

InterPro; IPR004000; Actin.

InterPro; IRR04000; Actin.
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Pred. No. 5.1e-06;
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PROSITE; PS00406; ACTINS_1; 1.
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GRPRHQGVMVGMGQK 15
                                         37 GRPRHQGVMVGMGQK 51
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nes 15; Conservative
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                                                                                                                                                                                       RESULT 12
Q9QZB4
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Q86SB7
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Lytechinus variegatus (Sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Temnopleuroida; Toxopneustidae;
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-!- SIMILARITY: Belongs to the actin family.

BMBL, AB087882; BAC55093.1; -.

HSSP; P02577; INM1.

GO, GO:0005884; C:actin filament; IEA.

GO; GO:0003774; F:motor activity; IEA.

GO; GO:0003774; F:motor activity; IEA.

INCEPTO: IPR004001; Actin.

InterPro: IPR004001; Actin.

InterPro: Actin.

PRINTS; PR00190; ACTIN.

PROSTIN: PS00005, Actin.

PROSTIN: PS00046; ACTIN.

PROSTIN: PS00046; ACTIN.

PROSTIN: PS00046; ACTIN.

PROSTIN: PS00046; ACTINS.
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GO; GO:0003774; F:motor activity; IEA.
GO; GO:00002700; F:muctural constituent of cytoskeleton; IEA.
InterPro; IPR00401; Actin.
InterPro; IPR004000; Actin.like.
                                                                                                                                                                                                                                                                                                             100.0%; Score 82; DB 2; Length 104; 100.0%; Pred. No. 5.3e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               108 AA; 12094 MW; F670CB8A6CBD3AEA CRC64;
                                                                                                                                                                                                                                                                     SEQUENCE 104 AA; 11511 MW; 332777A2B08669B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JAN-1998 (TrEMBLrel. 05, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) Cytoplasmic actin LvC4 (Fragment).
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100.0%; Pred. No. 5.5e-06;
tive 0; Mismatches 0;
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PROSITE; PS01132; ACTINS_ACT_LIKE; 1.
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                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.
Matches 15; Conservative
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Pfam; PF00022; Actin; J
PRINTS; PR00190; ACTIN
                                                                                                                                                                                                                             Structural protein.
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nes 15; Conserv
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Lytechinus variegatus (Sea urchin).
Bukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Temnopleuroida; Toxopneustidae;
Vytechinus.
NCBI_TaxID=7654;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO; GO:0005884; C:actin filament; IEA.
GO; GO:0003774; F:motor activity; IEA.
GO; GO:0003770; F:motor activity; IEA.
InterPro; IPR004001; Actin_like.
InterPro; IPR004000; Actin_like.
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108 AA; 12097 MW; F670D62101164AEA CRC64;
                                                                                                                                                                                             01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Cytoplasmic actin LvC2 (Fragment)
                                                                                                                                  108 AA.
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                                                                                                                      PRELIMINARY;
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Search completed: April 8, 2005, 12:03:06 Job time : 57.8667 secs

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Compugen Ltd.
GenCore version (c) 1993 - 2005
         Copyright
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OM protein - protein search, using sw model

8, 2005, 09:58:56; Search time 62.4 Seconds (without alignments) 92.971 Million cell updates/sec April Run on:

US-09-423-351C-4 81 1 GGTTMYPGIADRMQK 15 Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 segs, 386760381 residues Searched:

2105692 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_16Dec04:* Database :

geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp2001ss:* geneseqp2003bs:* geneseqp2003bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Aaw92530 Beta-acti	18617 Novel hum	Aam81404 Human hae	Aam81907 Human hae	Abp42928 Human ova	Aau30705 Novel hum	13127 Human ova	Aam80875 Human hae	Aam81886 Human hae	Aam81332 Human hae	39047 Breast an	1 Human	Abu70816 Human adi	Adr09052 Human pro	3 Novel	70549 Human adi	Adi63068 Human apo	Abg15100 Novel hum	3011 Human apo	Abp98860 Human str	15323 Human pro	78101 Misgurnus	2	1532 Sequence	Aar50328 Drug resi
Desc	Aaw9	Abg0861	Aam8	Aam8	Abp4	Aau3	Abp4312	Aam8	Aam8	Aam8	Aab5904	Abo8477	Abu7	Adro	Abg0	Abu7054	Adi6	Abg1	Adi6	9dqW	Adm0532	Aay7810	Aab1298	Aap6153	Aars
ΙD	AAW92530	ABG08617	AAM81404	AAM81907	ABP42928	AAU30705	ABP43127	AAM80875	AAM81886	AAM81332	AAB59047	AB084771	ABU70816	ADR09052	ABG00383	ABU70549	AD163068	ABG15100	ADI63011	ABP98860	ADM05323	AAY78101	AAB12985	AAP61532	AAR50328
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Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
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Aaw59176 P. calini Aab15017 Posttrans Aay94569 Human car Abb77195 Human act Abr64271 Angiogene Abr62328 Pacific w Abm04810 Rat Cytop Adb85212 Rat actin Adb85212 Rat actin Adb85212 Rat actin Adb85212 Rat actin Adb85210 Rat proce Adi63062 Human apo Adi63040 Human apo Adi6290 Human apo Adi770489 Actin pro Adi7103 Human apo Adi7103 Human apo Adi7103 Human apo Adi7103 Human apo Adi7103 Human apo Adi7103 Human apo Adi7103 Human apo Adi77048 Actin pro Adi77048 Actin pro Adi7704 Human ara Ady86098 Gamma 1 a Abo84772 Human can Abo84772 Human can	
AAM59176 AAN915017 AAN94569 ABN7395 ABR64271 ABR64271 ABR64270 ADB85212 ADB61174 ADF13052 ADI63040 ADI63040 ADI63040 ADI63040 ADI73062 ADI73002 ADI7331 ADP12391 ABN80841	
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ALIGNMENTS

Peptide substrate; CCT; eukaryotic type II chaperonin complex; cyclin; biding agent; substrate-binding site; SBS; substrate folding; actin; tubulin; treatment; cancer; anticancer drug; viral infection; screening; reduced toxicity. Beta-actin reference peptide substrate #4. AAW92530 standard; peptide; 15 AA. (first entry) 26-APR-1999 AAW92530; RESULT 1 AAW92530

Synthetic.

WO9853322-A1

26-NOV-1998.

98WO-GB001485. 22-MAY-1998; 97GB-00010762. 23-MAY-1997; (CANC-) INST CANCER RES ROYAL CANCER HOSPITAL.

Liou AK; Hynes G, Willison K,

WPI; 1999-070162/06.

Identifying specific binding agents for substrate binding site in CCT chaperonin complex - also new peptide binding agents and their mimetics, and peptides containing a specific CCT binding site, used for treating cancer.

Disclosure; Fig 10; 97pp; English.

This invention describes a method which uses the CCT (eukaryotic type II chaperonin) complex or part of it, for identifying a binding agent that can occupy a substrate-binding site (SBS) on the CCT complex. By binding to the CCT complex, the binding agents block an SBS so that biological activity of the CCT complex is affected, particularly its ability to fold substrates such as actin, tubulin and cyclin. The binding agents are useful for trearment of cancer, particularly when used in combination with an anticancer drug, or viral infections. Nucleic acid fragments are used to screen for agents, e.g. binding agents that modulate interaction between the CCT complex and a protein that is to be folded. The binding

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PGK) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed sequence tags for identifying expressed sequence tags that it is useful in gene therapy techniques to restore normal setuity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences ABG00010-ABG30377 represent novel human diagnostic maino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in
                                                                                                                                                                                  ö
                        80
                                                                                                                                                                                    Gaps
agents may target cells that are actively synthesising tubulin etc. Unlike known microtubule-stabilising agents that affect all cells) should have reduced toxicity for normal cells. AAW92527-W92541 are peptide substrates used in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human, chromosome mapping, gene mapping, gene therapy, forensic,
food supplement, medical imaging, diagnostic, genetic disorder.
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0
                                                                                                                                          Length 15;
                                                                                                                                        Score 81; DB 2; Length 15
Pred. No. 3.4e-07;
Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel human diagnostic protein #8608.
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                                                                                                                                100.0%; Sco
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                              ABG08617 standard; protein; 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
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                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 15; Conservative
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                                                                                                   Sequence 15 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Compositions and methods for the detection of hematological malignancies, e.g. chronic lymphocytic leukemia, lymphoma, follicular lymphoma and Hodgkin's and T/B cell non-Hodgkin's lymphoma.
                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                      Human, cytostatic, vascular, gene therapy, vaccine, lymphoma, haematological malignancy, antigen, chronic lymphocytic leukaemia, follicular lymphoma, Hodgkin's lymphoma,
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                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                            Human haematological malignancy-related antigen #1102.
                                                                        Score 81; DB 4; I
Pred. No. 2.2e-06;
                                                                                                      Mismatches
electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                       AAM81404 standard; protein; 100 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-MAR-2000; 2000US-0190479F.
27-APR-2000; 2000US-0200545F.
28-APR-2000; 2000US-0200303P.
28-APR-2000; 2000US-0200739F.
01-MAY-2000; 2000US-0200999F.
                                                                       100.0%;
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14-JUL-22000; 2000US-0218950P.
03-AUG-2000; 2000US-0222903P.
04-AUG-2000; 2000US-0223416P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2001; 2001WO-US007272.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-AUG-2000; 2000US-0223378P
                                                                                                                                  15
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                                                                                                      15; Conservative
                                                                                                                                  1 GGTTMYPGIADRMOK
                                                                                                                                                              GGTTMYPGIADRMOK
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                                                                     Query Match
Best Local Similarity
                                           Sequence 86 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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Indels

Pred. No. 2.6e-06; Mismatches 0;

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100.0%; Score 81; DB 4; Length 100;
Query Match
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Compositions and methods for the detection of hematological malignancies, e.g. chronic lymphocytic leukemia, lymphoma, follicular lymphoma and Hodgkin's and T/B cell non-Hodgkin's lymphoma.
                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             haematological malignancy; antigen; chronic lymphocytic leukaemia;
follicular lymphoma; Hodgkin's lymphoma; non-Hodgkin's lymphoma.
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                                                    Length 100;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human haematological malignancy-related antigen #1605.
                                                      Score 81; DB 4; I Pred. No. 2.6e-06;
                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                             AAM81907 standard; protein; 100 AA
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28-APR-2000; 2000US-020079P.
01-MAY-2000; 2000US-020099P.
04-MAY-2000; 2000US-0202084P.
14-JUL-2000; 2000US-021850P.
03-AUG-2000; 2000US-021850P.
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100.0%;
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                                                                                                                                                                 1 GGTTMYPGIADRMQK 15
                                                                                                                                                                                                                GGTTMYPGIADRMOK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                    Query Match 100.
Best Local Similarity 100.
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-514842/56.
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Sequence 100 AA;
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The invention relates to 2175 novel human ovarian antigens (ABB41054-ABB43228) and to cDNAs encoding them (ABG54131-ABG56305), and also encompasses polypeptides 90% identical and polynucleotides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigen to polynucleotides, antibodies against human ovarian antigens and the use of ovarian intigens of polynucleotides and polypeptides in diagnosing, treating prognosing or preventing various ovary and/or breast cancer, and disorders. Such conditions include ovarian cancer and breast cancer, and metastatic tumours of ovarian or breast of pregnancy, anovulation, disorders (e.g., infertility, disorders of pregnancy, anovulation, collisorders (e.g., infertility, disorders of pregnancy, anovulation, oplycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic conspinitis), immune disorders (e.g., conganital and acquired immunodeficiencies, autoimmune ophoritis, systemic lupus erythematosus, respiratory disorders (e.g., anaemia), cardiovascular disorders, respiratory disorders, neurological disorders, respiratory disorders, neurological disorders, respiratory system disorders. Ovarian antigen polypeptides and urinary system disorders. Ovarian antigen polypeptides and compounds which
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and neurological diseases.
                                                                                                                                                                                                                                                                                                                                                                     Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour; ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovalation; polycystic ovary syndrome; PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; infection; cardiovascular disorder; respiratory disorder; neurological disorder; gestrointestinal disorder; urinary system disorder; drug screening; gene therapy; chromosome mapping; forensic analysis; antibody preparation; cytoscatic; immunomodulatory; neuroprotective; antiinflammatory; gynaecological; reproductive.
  Gaps
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                                                                                                                                                                                                                                                                                                                              Human ovarian antigen HPDRS46, SEQ ID NO:4060.
Mismatches
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                                                                                                                                                                                                  ABP42928 standard; protein; 110 AA.
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                                                                           46 GGTTMYPGIADRMQK 60
                                                                                                                                                                                                                                                                                       (first entry)
  15; Conservative
                                             1 GGTTMYPGIADRMOK
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                                                                                                                                                                                                                                                                                       22-AUG-2002
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The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapentic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to encoding the polypeptides and cells genetically engineered to everyees them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon cand/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid sequences of novel human
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modulate ovarian antigen expression or activity. The polynucleotides may further be used for gene therapy, chromosome mapping, in the identification of individuals and in forensic analysis, and the polypeptides may be used as food additives or to prepare antibodies useful in disease diagnosis, drug targeting and phenotyping. The present sequence represents a human ovarian antigen of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; vaccination; gene therapy; nutritional supplement;
stem cell proliferation; haematopoiesis; nerve tissue regeneration;
immune suppression; immune stimulation; anti-inflammatory; leukaemia.
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                                                                                                                                                                                                                                                   Score 81; DB 5; Length 110; Pred. No. 2.9e-06;
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                                                                                                                                                                                                                              100.0%; Scor.
100.0%; Pred. No. 2..
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU30705 standard; protein; 118 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel human secreted protein #1196.
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                                                                                                                                                                                                                                                                                                                                       1 GGTTMYPGIADRMQK 15
                                                                                                                                                                                                                                                                                                                                                              36 GGTTMYPGIADRMQK 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                            15, Conservative
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                                                                                                                                                                                                                                                                           Local Similarity
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                                                                                                                                                                                                             Sequence 110 AA;
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The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP4328) and to cDNAs encoding them (ABQ54131-ABQ56305), and also encompasses polypeptides 99% identical and polynucleotides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigens to polynucleotides, antibodies against human ovarian antigens, and the use of ovarian antigen polynucleotides and polypeptides in diagnosing, treating, prognosing or preventing various ovary and/or breast-related disorders Such conditions include ovarian cancer and breast cancer, and metastatic tumours of ovarian or breast origin, reproductive system disorders (e.g., infertility, disorders of pregnancy, anovulation, polycystic ovary syndrome, ovarian cysts, and dysmenorrhoes), endocrine chock syndrome, inflammatory conditions (e.g., mastitis, oophoritis and vaginitis), immune disorders (e.g., congenital and acquired
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                                                                                                                                                                                                                                                                                                                                                                                                                       Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour; ovarian cancer; breast cancer; tumour; reproductive system disorder; nifertility; pregnancy disorder; anovulation; polycystic ovary syndrome; PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disorder; urinary system disorder; drug screening; gene therapy; chromosome mapping; forensic analysis; antibody preparation; cytostatic; immunomodulatory; neuroprotective; antiinflammatory; gynaecological; reproductive.
                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            useful in the prevention, treatment and diagnosis of cancer (e.g. ov.
cancer), immune disorders, cardiovascular disorders and neurological
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                                                                       Length 118;
                                                                                                        Indels
                                                                       Score 81; DB 4; I Pred. No. 3.1e-06;
                                                                                                                                                                                                                                                                                                                                                                                          Human ovarian antigen HVVBD91, SEQ ID NO:4259.
                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                            ABP43127 standard; protein; 145 AA
secreted proteins of the invention
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                                                                                                                                                                                  26
                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                            Conservative
                                                                                                                                               1 GGTTMYPGIADRMQK
                                                                                                                                                                                42 GGTTMYPGIADRMOK
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                                                                                       Local Similarity
Les 15; Conserv
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                                  Sequence 118 AA;
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immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus), blood-related disorders (e.g., anaemia), cardiovascular disorders, acepiratory disorders, neurological disorders, gastrointeetinal disorders and urinary system disorders. Ovarian antigen polypeptides and polymucleotides may also be used in screening for compounds which modulate ovarian antigen expression or activity. The polymucleotides may further be used for gene therapy, chromosome mapping, in the identification of individuals and in forensic analysis, and the polypeptides may be used as food additives or to prepare antibodies useful in disease diagnosis, drug targeting and phenotyping. The present sequence represents a human ovarian antigen of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Compositions and methods for the detection of hematological malignancies, e.g. chronic lymphocytic leukemia, lymphoma, follicular lymphoma and Hodgkin's and T/B cell non-Hodgkin's lymphoma.
                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, cytostatic, vascular, gene therapy, vaccine, lymphoma,
haematological malignancy, antigen, chronic lymphocytic leukaemia,
follicular lymphoma, Hodgkin's lymphoma, non-Hodgkin's lymphoma.
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                                                                                                                                                                                                                                                                      Length 145;
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                                                                                                                                                                                                                                                                    Score 81; DB 5; I
Pred. No. 3.9e-06;
                                                                                                                                                                                                         ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                            AAM80875 standard; protein; 147 AA.
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2000US - 0200779P.
2000US - 02002084P.
2000US - 0202084P.
2000US - 020201P.
2000US - 0218950P.
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                                                                                                                                                                                                                                                                                                                                                  71 GGTTMYPGIADRMQK 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
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                                                                                                                                                                                                                                       Sequence 145 AA;
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04-MAY-2000;
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           detection, diagnosis and therapy of haematological malignancies. The present sequence is the protein sequence of a human haematological malignancy related antigen. The methods of the present invention comprise detecting the presence of haematological malignancy related antigen (s) in a sample obtained from the patient (an increased level of the polypeptide, compared to an unaffected individual, is indicative of an increased risk). Haematological malignancies which can be treated using the present invention are chronic lymphocytic leukaemia, lymphoma, follicular lymphoma, Hoddkin's lymphoma, non-Hoddkin's lymphoma and T/B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human, cytostatic, vascular, gene therapy, vaccine, lymphoma,
haematological malignancy, antigen, chronic lymphocytic leukaemia,
follicular lymphoma, Hodgkin's lymphoma, non-Hodgkin's lymphoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to compositions and methods for the detection, diagnosis and therapy of haematological malignancies. The present sequence is the protein sequence of a human haematological
present invention relates to compositions and methods for the
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                                                                                                                                                                                                                     100.0%; Score 81; DB 4; Length 147; 100.0%; Pred. No. 4e-06; ive 0; Mismatches 0; Indels
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2000US-0200545P.
2000US-0200303P.
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2000US-0206201P.
2000US-0218950P.
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2000US-0223416P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000US-0223378P
                                                                                                                                                                                                                                                                                       1 GGTTMYPGIADRMQK 15
                                                                                                                                                                                                                                                                                                        cell non-Hodgkin's lymphoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-NOV-2001 (first entry)
                                                                                                                                                                                                                                                        15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-514842/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                         Sequence 147 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200164886-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-APR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2000;
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01-MAY-2000;
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                                                                                                                                                                                                                                                                                                                     73
                                                                                                                                                                                                                       Query Match
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malignancy related antigen. The methods of the present invention comprise detecting the presence of haematological malignancy related antigen(s) in a sample obtained from the patient (an increased level of the polypeptide, compared to an unaffected individual, is indicative of an increased risk). Haematological malignancies which can be treated using the present invention are chronic lymphocytic leukaemia, lymphoma, follicular lymphoma, Hodgkin's lymphoma, non-Hodgkin's lymphoma and T/B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to compositions and methods for the detection, diagnosis and therapy of haematological malignancies. The present sequence is the protein sequence of a human haematological malignancy related antigen. The methods of the present invention comprise detecting the presence of haematological malignancy related antigen(s) in a sample obtained from the patient (an increased level of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Compositions and methods for the detection of hematological malignancies, e.g. chronic lymphocytic leukemia, lymphoma, follicular lymphoma and Hodgkin's and T/B cell non-Hodgkin's lymphoma.
                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; cytostatic; vascular; gene therapy; vaccine; lymphoma;
haematological malignancy; antigen; chronic lymphocytic leukaemi
follicular lymphoma; Hodgkin's lymphoma; non-Hodgkin's lymphoma.
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                                                                                                                                                                                    Length 147;
                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human haematological malignancy-related antigen #1030.
                                                                                                                                                                                    Score 81; DB 4;
Pred. No. 4e-06;
                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                   AAM81332 standard; protein; 147 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mannion J
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27-APR-2000; 2000US-0200545F.
28-APR-2000; 2000US-0200739F.
01-MAY-2000; 2000US-0200779F.
04-MAY-2000; 2000US-020099F.
22-MAY-2000; 2000US-0202084F.
                                                                                                                                                                                    100.0%;
100.0%;
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                                                                                                                   cell non-Hodgkin's lymphoma
                                                                                                                                                                                                                                                  1 GGTTMYPGIADRMQK 15
                                                                                                                                                                                                                                                                                 GGTTMYPGIADRMOK 87
                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaiger A, Algate PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-514842/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CORI-) CORIXA CORP.
                                                                                                                                                   Sequence 147 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200164886-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-AUG-2000;
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AAM81332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Breast and ovarian cancer associated antigen protein sequence SEQ ID 755.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New human breast and ovarian cancer associated gene sequences and the polypeptides encoded by these genes, useful in the prevention, treatment and diagnosis of cancer, immune disorders, cardiovascular disorders and neurological diseases.
polypeptide, compared to an unaffected individual, is indicative of an increased risk). Haematological malignancies which can be treated using the present invention are chronic lymphocytic leukaemia, lymphoma, follicular lymphoma, Hodgkin's lymphoma and T/B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive; noctropic; neurpprotective; antiviral; antiallergic; hepatotropic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; immune disorder; Addison's disease; allergy; autoimmune haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; Crohn's disease; multiple sclerosis; rheumatoid arthritis; ulcerative colitis; cardiovascular disorder; wound healing; neurological disease.
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                                                                                                                                   100.0%; Score 81; DB 4; Lengtu ...
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                                                                                                                                                                                                                                                                                                                                                                                  AAB59047 standard; protein; 148 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-MAR-2000; 2000WO-US005881.
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                                                                                                                                                                                                                                             15
                                                                                   cell non-Hodgkin's lymphoma
                                                                                                                                                                                                                                                                                   87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-MAR-2001 (first entry)
                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                   73 GGTTMYPGIADRMOK
                                                                                                                                                                                                                                             1 GGTTMYPGIADRMQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-611515/58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rosen CA, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAF21950.
                                                                                                                          Sequence 147 AA;
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                                                                                                                                                                                                                                                                                                                                             RESULT 11
AAB59047
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Gaps

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Mismatches

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Conservative

15;

Matches

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The invention relates to cancer-associated proteins (CAP) and the cancer-associated (CAP) nucleic acids encoding them. The invention also relates to a method for treating cancers involving administering to a patient and inhibitor of CAP, and a method of screening for anticancer activity in a contential drug involving providing a cell that expresses a CA gene, contenting at issue sample derived from a cancer cell with an anticancer drug candidate on expression of the CA gene. The CAP proteins are useful for detecting cancer associated with expression of a CAP protein in a test cell sample and for screening for a bioactive agent capable of modulating the activity of a CAP protein. The CA nucleic acids are useful for diagnosing cancer, involving determining the expression of a CA nucleic acid in a tissue. This sequence represents a human CAP of the invention. Note: The sequence data for this patent did not form part of the printed cape specification, but was obtained in alectronic format directly from WIPO.
                                                                                                                                                                                       ö
               haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's diabeae, multiple sclerosis, rheumatoid arthritis and ulocrative colitis; cardiovascular disorders such as myocardial ischaemias; wound healing; neurological diseases such as cerebral anoxia and epilepsy; and
                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel human cancer associated protein encoded within open reading f
of cancer associated gene, useful as targets for diagnosing cancer.
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0
                                                                                                                                                      Score 81; DB 3; Length 148; Pred. No. 4e~06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; cancer-associated protein; CAP; cancer; cytostatic
                                                                                                                                                                                     0; Indels
 Addison's disease, allergies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                Human cancer-associated protein (CAP) HP07-010.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 81; DB 8;
Pred. No. 4e-06;
                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 18; SEQ ID NO 66; 182pp; English.
                                                                                                                                                                                                                                                                                                                                          ABO84771 standard; protein; 149 AA.
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0
                                                                                                                                                      100.0%;
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                                                                                                                                                                                                                         15
                                                                                                                                                                                                                                                       19 GGTTMYPGIADRMOK 33
                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                         1 GGTTMYPGIADRMQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Morris DW, Malandro MS;
                                                                                                                                  Query Match
Best Local Similarity
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disorders
                                                                                    infectious diseases
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Best Local Similarity
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                                                                                                                    Sequence 148 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO2004058146-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                             18-NOV-2004
   immune
                                                                                                                                                                                                                                                                                                                                                                           AB084771;
                                                                                                                                                                                                                                                                                                          RESULT 12
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Length 149;

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The inversion relates to a complex between two interacting processing the inversion relates to a complex between two interacting about protein from a known adipocyte marker and then by selecting a bait protein from a known adipocyte marker and then complex of an adipocyte cDNA library. The proteins are designated SID complex of an adipocyte cDNA library. The proteins are designated SID complex of an adipocyte cDNA library proteins. Also included are a recombinant host cell expressing at least one of the interacting oplymeptides of the complex, selecting a modulating compound in adipocyte cells, a recombinant host cell expressing at least one of the interacting polymeptides of the complex, selecting a modulating compound in adipocyte cells, a SID (RTM) polymeptide comprising any of the 738 amino acid a SID (RTM) polymucleotide comprising any of the 738 mucleotide sequences given in the specification (including its fragment or variant), a vector comprising the vector, a protein chip comprising the polymeptides and compounds are useful for preventing or treating metabolic disorders such as obesity or diabetes. The polymucleotides are useful as probes or primers. The complex is particularly useful for identifying selected interacting domains (SID particularly useful for identifying selected interacting domains (SID particularly useful for preventing or treating or treating domains (SID particularly useful for particularly useful for identifying selected interacting domains (SID)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for screening drugs that modulate the protein interaction, thus
ting the therapeutic effect. The present sequence represents a SID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New complex between two interacting proteins in adipocyte cells, useful for identifying selected interacting domains that modulate protein interactions, or for preventing or treating metabolic disorders such as obesity or diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a complex between two interacting proteins in
                                                                                                                                                                                                                                                                                                                               Human, prey, adipocyte, SID, selected interacting domain, anorectic, antidiabetic, protein-protein interaction, diabetes, yeast 2-hybrid assay, metabolic disorder, obesity.
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                                                                                                                                                                                                                                                                                      Human adipocyte Selected Interacting domain, SID, #447.
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Pred. No. 5.4e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 6; Page 259-260; 382pp; English.
                                                                                                                                                     ABU70816 standard; protein; 196 AA.
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                                         89
1 GGTTMYPGIADRMQK 15
                                                                                                                                                                                                                                          (first entry)
                                           GGTTMYPGIADRMOK
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N-PSDB; ACA57360.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 196 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                          10-JUN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Legrain P,
                                         75
                                                                                                                                                                                              ABU70816;
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                                                                                                         RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New 1995 cDNA, useful for treating osteoporosis, neurological diseases, Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
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                                                                                                                                                                                                                                                                                                                                                                    human, oligo-capping method, diagnostic marker, gene therapy, osteoporosis; neurological disease, Alzheimer's disease, parkinson's disease, dementia; short memory; cancer; sense or motor function, emotional reaction, fear response; panic, osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Otsuki T;
  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention relates to novel, isolated full length human cDNA
                                                                                                                                                                                                                                                                                                                             Human protein useful for treating neurological disease Seq 2558.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 81; DB 8; Length 214; Best Local Similarity 100.0%; Pred. No. 5.9e-06; Matches 15; Conservative 0; Mismatches 0; Indels
  Indels
  ;
  Mismatches
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Nagai K, Irie R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 2558; 2686pp; English.
                                                                                                                                                                                                   ADR09052 standard; protein; 214 AA.
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09-MAY-2003; 2003JP-00131452.
                                                                        175 GGTTMYPGIADRMOK 189
                                             1 GGTTMYPGIADRMQK 15
                                                                                                                                                                                                                                                                                       (first entry)
  15; Conservative
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Wakamatsu A, Ishii S,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tranquiliser.
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                                                                                                                                                                                                                                                                                       04-NOV-2004
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at fixed by the patent did not appear is the sequence and the sequence for this patent did not appear in the printed specification, but was obtained in fire.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel human diagnostic protein #374
                                                                                                                                                                                                                                                                                 ABG00383 standard; protein; 258 AA.
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23-AUG-2000; 2000US-00649167.
                                                 157 GGTTMYPGIADRMQK 171
1 GGTTMYPGIADRMOK 15
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Best Local Similarity 100.v
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Search completed: April 8, 2005, 10:50:43 Job time : 63.4 secs

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RESULT 2
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Sequence 731, App
Sequence 2, Appli
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Sequence 10409, A
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Sequence 5
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
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US-09-17-33A-7
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Sequence 10409, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-3
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
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                                          Sequence 2, Appli
Sequence 4, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 3566, Ap
Sequence 14623, Ap
Sequence 1555, Ap
Sequence 2, Appli
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Sequence 4, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 7725, Ap
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US-09-306-446C-6

i Sequence 6, Application US/09306446C

i Patent No. 6372559

i GENERAL INFORMATION:

i APPLICANT: KIM, Dong Soo

i APPLICANT: KIM, Chul Geun

i APPLICANT: NOH, Jae Koo

i PRETERENCE: P06344US0/BAS

i CURRENT APPLICATION NUMBER: US/09/306,446C

i CURRENT FILING DATE: 1999-05-06

i PRIOR APPLICATION NUMBER: KR 98/20255

i ROBER OF SEQ ID NOS: 33

i SEQ ID NOS: 33

i SEQ ID NOS: 33

i ENAMBER OF SEQ ID NOS: 33
                                                                                                                                                                                                                                                                             Sequence 1110,
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                                Sequence 3
Sequence 2
Sequence 4
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Pred. No. 5.9e-07;
Mismatches 0; Indels
          US-09-248-756A-14107
US-09-248-756A-14107
US-09-583-110-3667
US-08-378-213-2
US-08-378-213-4
US-09-120-044-3
US-09-120-044-3
US-09-902-540-14623
US-09-543-611A-8255
US-09-214-631-3
US-08-635-130A-4
US-08-635-130A-4
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US-09-538-092-1109
US-09-538-092-1110
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US-09-306-446C-6
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Best Local Similarity
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RESULT 4
US-09-306-446C-2
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                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/08609236
Patent No. 6087398
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 6
CORRESPONDENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: MGGregor & Adler, LLP
STREET: 8011 Candle Lane
CITY: Houston
STREET: Texas
COUNTRY: USA
ZIP: 77071
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                                                                                                                                             100.0%; Score 81; DB 4; Length 239; 100.0%; Pred. No. 2.7e-06;
                                                                                                                                                                                   0; Indels
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Apple Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word for Macintosh
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/609,236
CLASSIFICATION: 514
PRIOR APPLICATION: 514
PRIOR APPLICATION: 514
PRIOR APPLICATION: 514
APPLICATION NUMBER: 60/002,288
FILING DATE: August 14, 1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Benjamin Aaron Adler; Ph.D.
REGISTRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D5807
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-777-6908
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 374
WUNDER: Amino acid
                                                                                                                                                                                   0; Mismatches
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10409
LENGTH: 239
                                                                                                                                                                                                                                            165 GGTTMYPGIADRMQK 179
                                                                                                                                                                                                                    1 GGTTMYPGIADRMOK 15
                                                                                                                                             Query Match
Best Local Similarity 100.0
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
DESCRIPTION: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: Amino acid STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HYPOTHETICAL: NO ANTI-SENSE: NO FRAGMENT TYPE: ORIGINAL SOURCE:
                                                                                     ; ORGANISM: Human
US-09-949-016-10409
                                                                                                                                                                                                                                                                                                             RESULT 3
US-08-609-236-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-609-236-6
                                                                        TYPE: PRT
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DB 3; Length 374;

100.0%; Score 81;

Query Match

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APPLICANT: CHO, Kyou Nam
TITLE OP INVENTION: EXPRESSION VECTOR OF MUD LOACH GROWTH HORMONE GENE
FILE REFERENCE: P0634440180/BAS
CURRENT APPLICATION NUMBER: US/09/306,446C
CURRENT FILING DATE: 1999-05-06
PRIOR APPLICATION NUMBER: KR 98/20255
PRIOR APPLICATION NUMBER: KR 98/20255
PRIOR FILING DATE: 1998-06-01
NUMBER OF SEQ ID NOS: 33
SOFTWARE PATENT NOS: 2.0
SEQ ID NO 2
LENGTH: 374
                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 374;
                    Indels
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COUNTRY: U.S.A. ZOO. COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATCHTIN Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/106,217
Best Local Similarity 100.0%; Pred. No. 4.4e-06; Matches 15; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 81; DB 3; L
Best Local Similarity 100.0%; Pred. No. 4.4e-06;
Matches 15; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Saxe, Stephen A.
REGISTRATION NUMBER: 38,609
REFERENCE/DOCKET NUMBER: 2323-125
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                               ; Sequence 2, Application US/09306446C; Patent No. 6372959; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Misgurnus mizolepus
US-09-306-446C-2
                                                                                                  300 GGTTMYPGIADRMOK 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       300 GGTTMYPGIADRMOK 314
                                                           1 GGTTMYPGIADRMQK 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GGTTMYPGIADRMQK 15
                                                                                                                                                                                                                                                     APPLICANT: KIM, DONG SOO APPLICANT: KIM, Chul Geun APPLICANT: NAM, YOON KWON APPLICANT: NOH, Jae KOO APPLICANT: CHO, Kyou Nam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: Tower
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION:
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APPLICANT: USBYER, J. Craig et al.

APPLICANT: USBYER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOO1307

CURRENT PILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08
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Patent No. 6063576
GENERAL INFORMATION:
APPLICANT: Claon, Timothy M.
TITLE OF INVENTION: Actin Mutations in Dilated
TITLE OF INVENTION: Cardiomyopathy, a Heritable Form of Heart Failure
NUMBER OF SEQUENCES: 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 81; DB 1; Length 376; 100.0%; Pred. No. 4.4e-06;
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6100, Application US/09949016
Patent No. 6812339
                                                                                                  ATTORNEY/AGENT INPORMATION:
NAME: Ralph, Rebecca L.
REGISTRATION NUMBER: 35,152
REFERENCE/DOCKET NUMBER: TUU-
TELECOMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEPASK: 215-568-3439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      302 GGTTMYPGIADRMOK 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   302 GĞTTMYPGIADRMQK 316
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Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15; Conservative
                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 376 amino acids
                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                    CLASSIFICATION: 436
                                    APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-949-016-6100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRICANT: FUTNESS, Michael
APPLICANT: Buchbinder, Jenny
APPLICANT: Buchbinder, Jenny
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
FILE REFERENCE: PA-0041 US
CURRENT APPLICATION NUMBER: uS/09/976,594
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 60/240,409
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 1143
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                                                                                                                                                                                                                  Length 375;
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                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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APPLICANT: McHugh, Kirk M.

TITLE OF INVENTION: DIAGNOSTIC TEST FOR DETERMINING

TITLE OF INVENTION: MALIGNANCY OF SMOOTH MUSCLE TUMORS

VUMBER OF SEQUENCES: 4

CORRESPONDENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &

ADDRESSEE: No. 5710003zis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6673549 1837317CD1
                                                                                                                                                                                                                                         4.4e-06;
                                                                                                                                                                                                                                                              Mismatches
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STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-976-594-731
Sequence 731, Application US/09976594
Patent No. 6673549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/08588113
Patent No. 5710003
                                                                                                                                                                                                                                                                ;
0
                                      INFORMATION FOR SEQ ID NO: 16: SEQUENCE CHARACTERISTICS: LENGTH: 375 amino acids TYPE: amino acid
                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0%;
Matches 15; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 GGTTMYPGIADRMOK 315
                                                                                                                                                                                                                                                                                                                                       301 GGTTMYPGIADRMOK 315
                                                                                                                                                                                                                                                                                                         1 GGTTMYPGIADRMOK 15
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202-783-6040
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Matches 15; Conservative
                                                                                                                                                , MOLECULE TYPE: protein US-09-106-217-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-976-594-731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 731
LENGTH: 375
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; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7721
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                                        US-09-917-254-53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
               ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
STREET: 555 Thirteenth Street, N.W., Suite 701 East
STREET: Tower
                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673545 1709118CD1
US-09-919-172-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 81; DB 4; I 100.0%; Pred. No. 4.4e-06; trive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 81; DB 3; 1 Pred. No. 4.4e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 10
US-09-919-172-33

Sequence 33, Application US/09919172

Patent No. 6673545

GENERAL INFORMATION:
APPLICANT: Faris, Mary
TITLE OF INVENTION: PROSTATE CANCER WARKERS
FILE REFERENCE: PA-0036 US
CURRENT FILING DATE: 2001-07-30

PRIOR PILING DATE: 2001-07-30

PRIOR PILING DATE: 2000-07-28

NUMBER OF SEQ ID NOS: 102

SOFTWARE: PERL PROGRAM

SEQ ID NO 33

LENGTH: 377

TYPE: PRT

ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                       APPLICALL.

APPLICALL.

FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Saxe, Stephen A.
REGISTRATION NUMBER: 38,609
REFERENCE/DOCKET NUMBER: 2323-125
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-783-6040
"""TELEPHONE: 202-783-6040
"""" OF THE TELEPHONE: 202-783-6040
""" OF THE TELEPHONE: 202-783-6040
                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/106,217
                                                                                                                        ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0%;
Matches 15; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 202-783-6031
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  303 GGTTMYPGIADRMQK 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GGTTMYPGIADRMOK 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 377 amino acids
amino acid
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Best Local Similarity 100.
Matches 15; Conservative
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
                                                                          Washington
                                                                                                         U.S.A.
                                                                        CITY: Was
STATE: DC
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-106-217-2
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303 GGTTMYPGIADRMOK 317

1 GGTTMYPGIADRMQK 15

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Sequence 7121, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE PEPERENCE: CL001307
CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

NUMBER: OF SEQ ID NOS: 207012

SEQ ID NO 7721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9424, Application US/09949016;
Patent No. 6812139;
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
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                                       GENERAL INFORMATION:

APPLICANT: Mutter, George
APPLICANT: Baak, Jan
TITLE OF INVENTION: Prognostic Classification of Breast Cancer
FILE REFERENCE: B0801/7224 (JRV)
CURRENT APPLICATION NUMBER: US/09/917,254
CURRENT FILING DATE: 2000-07-27
PRIOR APPLICATION NUMBER: US 60/222,093
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 102
SOFTWARE: PatentIn version 3.0
SEQ ID NO 53
LENGTH: 377
THER: PRI
ORGANISM: Homo Sapiens
US-09-917-254-53
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Sequence 53, Application US/09917254
Patent No. 6703204
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Best Local Similarity 100.0
Matches 15; Conservative
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Best Local Similarity 100.
Matches 15; Conservative
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GENERAL INFORMATION:
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GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
CURRENT FILING DATE: 2000-04-14
FRIOR APPLICATION NUMBER: 60/241,755
FRIOR APPLICATION NUMBER: 60/241,755
FRIOR PELLING DATE: 2000-10-03
FRIOR PELLING DATE: 2000-10-03
FRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOPTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 10757
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Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
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Pred. No. 4.7e-06;
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100.0%; Score 81; DB 4; I
Best Local Similarity 100.0%; Pred. No. 4.7e-06;
Matches 15; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                 CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-0-06
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PSECSE for Windows Version 4.0
SSOFTWARE: 7994
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Patent No. 6812339
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Best Local Similarity 100.0%;
Matches 15; Conservative 0
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FILE REFERENCE: CL001307
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US-09-949-016-9424
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US-09-949-016-10757
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US-09-949-016-10757
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## PRIOR APPLICATION NUMBER: 60/237,768
### PRIOR FILING DATE: 2000-10-03
### PRIOR FILING DATE: 2000-10-03
### PRIOR FILING DATE: 2000-09-08
### PRIOR PRIOR DATE: 2000-09-09-09
### PRIOR PRIOR DATE: 2000-09-09
### PRIOR PRIOR DATE: 2000-09
### PRIOR DATE: 2000-09
### PRIOR PRIOR DATE: 20
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Search completed: April 8, 2005, 12:07:35 Job time : 18.5333 secs

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April 8, 2005, 10:53:18; Search time 42.6667 Seconds (without alignments) 116.718 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT WW PUBL pep:*

2: /cgn2_6/ptodata/1/pubpaa/USO6_NEW PUBL pep:*

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10: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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81
1 GGTTMYPGIADRMQK 15
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Searched:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SUMMAKIES			
Result		Query	1	á		1		
. i	Score	Macch	match Length UB	3 :	di.	Description		:
П	81	100.0		0	US-09-796-692-1768	Sequence 1768,	768, 1	Ap
7	81	100.0		σ	US-09-796-692-2271	Sequence 2271,		đ
3	81	100.0		14	US-10-040-862-1768	Seguence 1768,	1768,	Ap
4	81	100.0		14	US-10-040-862-2271	Seguence	2271,	Αp
ហ	81	100.0		15	US-10-057-475B-1768	Sequence	1768,	Ap
y	81	100.0		15	US-10-057-475B-2271	Sequence	2271,	Ap
7	81	100.0	100	15	US-10-154-884B-1768	Sequence 1768, Ap	1768,	Ap
œ	81	100.0		15	US-10-154-884B-2271	Sequence	2271,	Ap
0	81	100.0		16	US-10-764-324-1768	Seguence	1768,	Ap
10	81	100.0		16	US-10-764-324-2271	Sequence	2271,	Ap
11	81	100.0		15	US-10-264-049-4060	Sequence	4060,	Αp
12	81	100.0		15	US-10-424-599-143033	Seguence	14303	ώ,
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Sequence 1239, Ap		Sequence 2250, Ap	Sequence 1239, Ap	Sequence 1696, Ap	Sequence 2250, Ap			.,		_	2250		1239	Sequence 1696, Ap	Sequence 2250, Ap	Sequence 755, App	Sequence 755, App	Seguence 206389,	4008	Sequence 68, Appl	93,	88	2436	94,	82,	101	33, 7	Sequence 64, Appl	4,	Sequence 63, Appl	1436
9 US-09-796-692-1239	9 US-09-796-692-1696	9 US-09-796-692-2250	14 US-10-040-862-1239	14 US-10-040-862-1696	14 US-10-040-862-2250	15 US-10-057-475B-1239	15 US-10-057-475B-1696	15 US-10-057-475B-2250	15 US-10-154-884B-1239	15 US-10-154-884B-1696	2	US-10	16 US-10-764-324-1239	US-10	16 US-10-764-324-2250	9 US-09-925-298-755	14 US-10-102-806-755	2	2	16 US-10-322-281-68		14 US-10-316-253-88		US-10	15 US-10-260-708-82		9 US-09-919-172-33		US-10-333	16 US-10-322-281-63	9 US-09-925-301-1436
147 9	147	147	147]	147 1	147 1	147]	147 1	147]	147]	147]	147 1	147]	147 1	147 1	147 1	148	148 1	236 1	342]	371 1	375 1	375 1	375 1	375 1	375 1	376 1	377 9	377 1	377 1	398]	413 9
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ALIGNMENTS

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RESULT 1

US-09-766-692-1768

Sequence 1768, Application US/09796692

SEMBRAL INPORMATION: Alexander Application Osign Osi
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APPLICANT: Galge, Paul A.

APPLICANT: Galge, Paul A.

APPLICANT: Mainton, Jane
APPLICANT: Coriax Corpositions and Methods for the Detection, Diagnosis and Therapy
TITLE OF INVENTION: Hematological Malignancies
CURRENT APPLICATION NUMBER: US/10/040,862
CURRENT APPLICATION NUMBER: US/10/040,862
CURRENT APPLICATION NUMBER: US 60/10/10/6
FRIOR APPLICATION NUMBER: US 60/200,303
FRIOR PLIING DATE: 2000-04-28
FRIOR APPLICATION NUMBER: US 60/200,303
FRIOR PLIING DATE: 2000-04-28
FRIOR PLIING DATE: 2000-04-28
FRIOR PLIING DATE: 2000-05-01
FRIOR PLIING DATE: 2000-05-04
FRIOR APPLICATION NUMBER: US 60/223,918
FRIOR REPLICATION NUMBER: US 60/223,918
FRIOR APPLICATION NUMBER: US 60/223,918
FRIOR PLIING DATE: 2000-08-07
FRIOR APPLICATION NUMBER: US 60/223,918
FRIOR APPLICATION NUMBER: US 60/223,918
FRIOR PLIING DATE: 2000-08-07
FRIOR 
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Publication No. US20030078396A1

Publication No. US20030078396A1

Publication No. US20030078396A1

APPLICANT: Algate, Paul A.

APPLICANT: Adjate, Paul A.

APPLICANT: Retter, Marc

APPLICANT: Retter, Marc

APPLICANT: Corixa Corporation

TITLE OF INVENTION: Hematological Malignancies

FILE REFERENCE: 014058-013520US

CURRENT APPLICATION NUMBER: US/10/040,862

CURRENT FILING DATE: 2001-11-06

PRIOR APPLICATION NUMBER: US/10/6186,126
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Best Local Similarity 100.0%; Pred. No. 2.6e-06;
Matches 15; Conservative 0; Mismatches 0;
                                                     Sequence 1768, Application US/10040862
Publication No. US20030078396A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GGTTMYPGIADRMQK 15
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                                                                                                                                                             APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
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; ORGANISM: Homo sapiens
US-10-040-862-1768
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GENERAL INFORMATION
GENERAL INFORMATION
APPLICATION
APPLICANT: Algate, Paul A
APPLICANT: Algate, Paul A
APPLICANT: Algate, Paul A
APPLICANT: Algate, Paul A
APPLICANT: Mannion, Jane
ITILE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
TITLE REFRENCE: 2077.0120
CURRENT APPLICATION NUMBER: 05/0193-01
PRIOR PLILING DATE: 2000-03-10
PRIOR PL
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PRIOR FILING DATE: 2000-08-07
NUMBER OF SEQ ID NOS: 9597
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1768
LENGTH: 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GGTTMYPGIADRMOK 15
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US-09-796-692-1768
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US-09-796-692-2271
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Best Local Similarity
Matches 15; Conserv
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RESULT 3

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GENERAL INCORMATICAL ALEXANDER

APPLICANT: Algate Paul A.

APPLICANT: Clapper. Jonathan David

APPLICANT: Clapper. Jonathan David

APPLICANT: Cariza Algate

APPLICANT: Cariza Data

APPLICANT: Cariza Corporation

ITILE OF INVENTION: Cempositions and Methods for the Detection, Diagnosis and Therapy

TITLE OF INVENTION: Hematological Malignancies

TITLE OF INVENTION: Hematological Malignancies

CURRENT APPLICATION NUMBER: US 6/136,126

PRIOR APPLICANTON NUMBER: US 60/200,506

PRIOR APPLICANTON NUMBER: US 60/200,506

PRIOR APPLICANTON NUMBER: US 60/200,303

PRIOR PLING DATE: 2000-04-28

PRIOR PLING DATE: 2000-05-01

PRIOR PLING DATE: 2000-05-01

PRIOR PLING DATE: 2000-05-01

PRIOR APPLICANTON NUMBER: US 60/202,084

PRIOR PLING DATE: 2000-05-01

PRIOR APPLICANTON NUMBER: US 60/202,094

PRIOR PLING DATE: 2000-08-03

PRIOR PLING DATE: 2000-08-03

PRIOR PLING DATE: 2000-08-03

PRIOR PLING DATE: US 00/202,094

PRIOR PLING DATE: US 00/202,094

PRIOR PLING: US 00/2
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                                                               PRIOR FILING DATE: 2000-05-22
PRIOR APPLICATION NUMBER: US 60/206,201
PRIOR FILING DATE: 2000-05-22
PRIOR PILING DATE: 2000-05-14
PRIOR PILING DATE: 2000-07-14
PRIOR PILING DATE: 2000-08-03
PRIOR PILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
SEQID NOS: 10979.
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1768
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APPLICATION NUMBER: US 60/202,084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2271, Application US/10057475B Publication No. US20040002068A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0
....hes 15, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CRGANISM: Homo sapiens
US-10-057-475B-1768
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CRGANISM: HOMO
US-10-057-475B-2271
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APPLICANT: Angare, Jonathan David
APPLICANT: Clapper, Jonathan David
APPLICANT: Clapper, Jonathan David
APPLICANT: Clapper, Jonathan David
APPLICANT: Crater, Nadia
APPLICANT: Carter, Lauren
APPLICANT: Carter, Lauren
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
TITLE OF INVENTION: Hematological Malignancies
TITLE OF INVENTION: Hematological Malignancies
TITLE OF INVENTION: Hematological
TITLE OF INVENTION: Hematological
TITLE OF INVENTION WIMBER: US 60/186,126
PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR PILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: US 60/200,303
PRIOR PILING DATE: 2000-04-28
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                                                           PRIOR PILLING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR APPLICATION NUMBER: US 60/200,303
PRIOR FILING DATE: 2000-04-28
PRIOR PILLING DATE: 2000-04-28
PRIOR PILLING DATE: 2000-05-01
PRIOR PILLING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: US 60/202,084
PRIOR APPLICATION NUMBER: US 60/202,084
PRIOR PILLING DATE: 2000-05-01
PRIOR PILLING DATE: 2000-05-22
PRIOR PILLING DATE: 2000-05-22
PRIOR PILLING DATE: 2000-05-22
PRIOR PILLING DATE: 2000-05-23
PRIOR PILLING DATE: 2000-05-04
PRIOR PILLING DATE: 2000-06-03
PRIOR PILLING DATE: 2000-08-04
PRIOR APPLICATION NUMBER: US 60/223,378
PRIOR PILLING DATE: 2000-08-04
PRIOR PILLING DATE: 2000-08-04
PRIOR PILLING DATE: 2000-08-07
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                                          ION NUMBER: US 60/190,479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GGTTMYPGIADRMQK 15
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Best Local Similarity 100.
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US-10-040-862-2271
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Sequence 1768, Application US/10764324

Sequence 1768, Application US/10764324

Publication No. US20040175739A1

GENERAL INFORMATION:

APPLICANT: Alexander

APPLICANT: Adject, Paul A.

APPLICANT: Adject, Paul A.

APPLICANT: Adject, Marc

APPLICANT: Retter, Marc

APPLICANT: Corixa Corpositions and Methods for the Detection, Diagnosis and Therapy

ITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy

ITLE OF INVENTION: Hematological Malignancies

FILE REFERENCE: 014058-013520US

CURRENT FILING DATE: 2004-01-23

PRIOR APPLICATION NUMBER: US/10/764,324

CURRENT FILING DATE: 2000-03-01

PRIOR PLING DATE: 2000-03-01

PRIOR PLING DATE: 2000-03-17

PRIOR PLING DATE: 2000-03-17

PRIOR PLING DATE: 2000-03-17

PRIOR PLING DATE: 2000-03-17

PRIOR PLING DATE: 2000-04-28

PRIOR PRIOR PLING DATE: 2000-04-28

PRIOR APPLICATION NUMBER: US 60/200, 303

PRIOR PLING DATE: 2000-04-28

PRIOR PRIOR PLING DATE: 2000-04-28

PRIOR APPLICATION DATE: 2000-04-28
                                   TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy TITLE OF INVENTION: Hematological Malignancies
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagn.
FILE REFERENCE: 014058-0135210S
CURRENT APPLICATION NUMBER: US/10/154,884B
CURRENT FILING DATE: 2002-05-23
FRIOR PRIDK APPLICATION NUMBER: US 60/186,126
FRIOR APPLICATION NUMBER: US 60/180,479
FRIOR FILING DATE: 2000-03-17
FRIOR PILING DATE: 2000-03-17
FRIOR PILING DATE: 2000-04-28
FRIOR FILING DATE: 2000-04-28
FRIOR PILING DATE: 2000-04-28
FRIOR APPLICATION NUMBER: US 60/200,779
FRIOR APPLICATION NUMBER: US 60/200,999
FRIOR PILING DATE: 2000-05-04
FRIOR FILING DATE: 2000-05-04
FRIOR PILING DATE: 2000-05-04
FRIOR FILING DATE: 2000-05-04
FRIOR PILING DATE: 2000-05-04
FRIOR PILING DATE: 2000-05-05
FRIOR APPLICATION NUMBER: US 60/218,950
FRIOR APPLICATION NUMBER: US 60/222,903
FRIOR APPLICATION NUMBER: US 60/222,903
FRIOR PILING DATE: 2000-07-14
FRIOR PILING DATE: 2000-07-14
FRIOR SEQ ID NUSS: 11290
FRIOR SEQ ID NOS: 11290
FROM FRIOR PILING DATE: 2000-08-03
FROM FRANCE: FASTESQ FOR WINDOWS: 11290
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APPLICATION NUMBER: US 60/200,999
FILING DATE: 2000-05-01
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PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: US 60/202,084
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-154-884B-2271
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APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Mannion, Jane
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
TITLE OF INVENTION: Hematological Malignancies
FILE REFERENCE: 014058-01352105
CURRENT APPLICATION NUMBER: US 60/186,126
PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR APPLICATION NUMBER: US 60/200,479
PRIOR APPLICATION NUMBER: US 60/200,455
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: US 60/200,799
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-05-01
PRIOR FILING DATE: 2000-05-04
PRIOR FILING DATE: 2000-05-04
PRIOR FILING DATE: 2000-05-04
PRIOR PLING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: US 60/220,903
PRIOR PLING DATE: 2000-05-04
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                                                                       Length 100;
                                                                                                                                               Indels
                                                                   Score 81; DB 15;
Pred. No. 2.6e-06;
                                                                                                                                                   0; Mismatches
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1768
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; Publication No. US20040005561A1
; GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
; APPLICANT: Manion, Jane
; APPLICANT: Manion, Jane
; APPLICANT: Retter, Marc W.
; APPLICANT: Corixa Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1768, Application US/10154884B
Publication No. US20040005561Al
GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Sco
100.0%; Pre
ntive 0; }
                                                               Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 15; Conservative 0;
                                                                                                                                                                                                                       1 GGTTMYPGIADRMQK 15
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Best Local Similarity 100.
Matches 15; Conservative
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US-10-154-884B-1768
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Sequence 143033, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lar Rosa Thomas J
APPLICANT: Cao Yongwei
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE SERRENCE: 38-21(53233) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 143033
LENGTH: 133
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/264,049

CURRENT FILING DATE: 2002-10-04

PRIOR APPLICATION NUMBER: PCT/US01/18569

PRIOR PILING DATE: 2001-06-07

PRIOR APPLICATION NUMBER: US 60/209,467

PRIOR PILING DATE: 2000-06-07

NUMBER OF SEQ ID NOS: 4360

SOFTWARE: Patentin Ver. 3.1

SEQ ID NO 4060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 110;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Clone ID: PAT_MRT3847_100172C.1.pep
US-10-424-599-143033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 81, DB 15; Best Local Similarity 100.0%; Pred. No. 2.9e-06; Matches 15; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                            ; Sequence 4060, Application US/10264049; Publication No. US20040005579A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36 GGTTMYPGIADRMQK 50
           46 GGTTMYPGIADRMQK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GGTTMYPGIADRMQK 15
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Best Local Similarity 100.0
Matches 15; Conservative
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US-10-264-049-4060
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ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-424-599-143033
                                                                                        RESULT 11
US-10-264-049-4060
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US-10-264-049-4259
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APPLICANT: Retter, Marc
APPLICANT: Retter, Marc
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
TITLE OF INVENTION: Hematological Malignancies
FILE REFERENCE: 014058-013520US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                      PRIOR APPLICATION NUMBER: US 60/206,201
PRIOR FILING DATE: 2000-05-22
PRIOR FILING DATE: 2000-05-22
PRIOR FILING DATE: 2000-07-14
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 10467
SOFTWARE: PastSEQ for Windows Version 3.0
LENGTH: 100
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SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT PELLICA UNUMBER: US/10/764,324

CURRENT PELLING DATE: 2004-01-23

PRIOR FILING DATE: 2004-01-23

PRIOR FILING DATE: 2001-11-06

PRIOR PELLING DATE: 2001-11-06

PRIOR PELLING DATE: 2000-03-01

PRIOR PELLING DATE: 2000-03-17

PRIOR PELLING DATE: 2000-03-17

PRIOR PELLING DATE: 2000-03-17

PRIOR PELLING DATE: 2000-04-27

PRIOR PELLING DATE: 2000-04-28

PRIOR PELLING DATE: 2000-06-01

PRIOR PELLING DATE: 2000-06-01

PRIOR PELLING DATE: 2000-05-01

PRIOR PELLING DATE: 2000-05-01

PRIOR PELLING DATE: 2000-05-01

PRIOR PELLING DATE: 2000-05-01

PRIOR PELLING DATE: 2000-05-04

PRIOR PELLING DATE: 2000-05-02

PRIOR PELLING DATE: 2000-05-02

PRIOR PELLING DATE: 2000-05-02
PRIOR FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: US 60/206,201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2271, Application US/10764324
Publication No. US20040175739A1
GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
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Matches 15; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
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GERREAL INCORANTION:
APPLICANT: Gaiger, Alexander
APPLICANT: Gaiger, Alexander
APPLICANT: Gaiger, Alexander
APPLICANT: Agaiger, Alexander
APPLICANT: Agaiger, Alexander
APPLICANT: Agaiger, Alexander
TITLE OF INVENTION: COMPOSITIONS AND NETHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
ITLE OF INVENTION: COMPOSITIONS AND NETHODS FOR THE DETECTION, DIAGNOSIS
CURRENT PLING DATE: 2001-03-01
FRIOR PELICATION NUMBER: 00/186,126
FRIOR PELICATION NUMBER: 60/200,425
FRIOR PELICATION NUMBER: 60/200,545
FRIOR PELICATION NUMBER: 60/200,999
FR
                Score 81; DB 9; Length 147; Pred. No. 4e-06;
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Pred. No. 4e-06;
Mismatches 0; Indels
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Job time : 43.6667 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1696, Application US/09796692
Publication No. US20020198362A1
GENERAL INFORMATION:
            Query Match
Best Local Similarity 100.0%;
Matches 15; Conservative 0
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Best Local Similarity 100.0%;
Matches 15; Conservative 0
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Sequence 1239 Application US/09796692
Publication No. UG20020198652A1
GENERAL INPORMATION:
APPLICANT: Galger, Alexander
TITLE OF INVENTION: UGANGERITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
TITLE OF INVENTION: HAMATICAGICAL MALIGARANCIES
TITLE OF INVENTION: UNMER: 60/190, 479
FRIOR APPLICATION NUMBER: 60/190, 479
FRIOR PELLOR DATE: 2000-03-01
FRIOR APPLICATION NUMBER: 60/1200, 545
FRIOR APPLICATION NUMBER: 60/200, 303
FRIOR FILING DATE: 2000-04-28
FRIOR APPLICATION NUMBER: 60/200, 303
FRIOR APPLICATION NUMBER: 60/200, 303
FRIOR APPLICATION NUMBER: 60/200, 304
FRIOR APPLICATION NUMBER: 60/220, 303
FRIOR APPLICATION NUMBER: 60/220, 304
FRIOR APPLICATION NUMBER: 60/220, 307
FRIOR A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) LOCATION: (3) 7
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-264-049-4259
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Pred. No. 3.9e-06;
; Mismatches 0;
                            CURRENT APPLICATION NUMBER: US/10/264,049
CURRENT FILING DATE: 2002-10-04
FRIOR APPLICATION NUMBER: PCT/US01/18569.
FRIOR FILING DATE: 2001-06-07
FRIOR PELING DATE: 2000-06-07
FRIOR FILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 4360
SOFTWARE: Patentin Ver: 3.1
SEQ ID NO 4259
LENGTH: 145
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1239
LENGTH: 147
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Best Local Similarity 100.0%;
Matches 15; Conservative 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: MISC FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
FILE REFERENCE: PA133P1
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; ORGANISM: Homo sapiens
US-09-796-692-1239
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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- protein search, using sw model OM protein April 8, 2005, 09:58:56 ; Search time 9.3333 Seconds (without alignments) 154.634 Million cell updates/sec Run on:

US-09-423-351C-4 Title:

81 1 GGTTMYPGIADRMQK 15 Perfect score: Sequence:

BLOSUM62 Scoring table: 283416 seqs, 96216763 residues Searched:

Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: pirl:* 2: pirl:* 3: pir2:* 4: pir4:* PIR 79:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		de			SUMMARIES	
Result No.	Score	Query Match	Query Match Length	DB	αı	Description
-	81	100.0	7.1	~	139393	alpha-actin - huma
7	81	100.0	100	~	S14851	actin - fruit fly
9	81	100.0	125	~	A26337	actin, skeletal mu
4	81	100.0	195	~	S39777	actin beta - pig (
S	81	100.0	213	N	A61043 .	actin CA15 - sea s
9	81	100.0	308	~	A03000	actin 3 - fruit fl
7	81	100.0	328	~	805430	beta -
80	81	100.0	349	~	B25819	, fetal
6	81	100.0	362	~	A26559	type 5,
10	81	100.0	374	-1	ATBOB	beta - b
11	81	100.0	374	-	ATBOG	1
12	81	100.0	374	7	JC5818	₩.
13	81	100.0	375	Н	ATBOSM	ņ
14	81	100.0	375	Н	ATRB	actin, skeletal mu
15	81	100.0	375	, -1	ATRIC	actin beta - rat
16	81	100.0	375	~	A48324	beta, c
17	81	100.0	375	~	ATCHB	beta -
18	81	100.0	375	-	ATHUB	actin beta - human
19	81	100.0	375	-	ATHUG	actin gamma 1 - hu
20	81	100.0	375	-4	ATMSB	actin beta - mouse
21	81	100.0	375	٦	ATMSG	
22	81	100.0	375	Н	ATRBB	actin beta, non-mu
23	81	100.0	375	7	S11222	actin gamma, cytos
24	81	100.0	375	~	S33386	-
25	81		375	~	S47897	н
26	81	100.0	375	7	A26836	
27	81	100.0	375	7	871125	actin beta-2, cyto
28	81	100.0	375	N	711	
29	81	100.0	375	7	871126	actin beta, cytoso

actin beta - goose actin alpha, cardi	actin - imperfect actin 7 - fruit fl	actin gamma, cytos actin gamma, smoot	actin 8 - fruit fl	Actin-1A - nematod	actin 87E - fruit	actin - fruit fly	actin gamma, enter	actin - pork tapew	actin 4 - Caenorha	actin 1 and actin	actin 2 - Caenorha	hypothetical prote
A55001 A54728	S03126 ATFF7	A43552 ATCHSM	ATFF8	A48449	S04538	JC1246	A40261	A44940	S27135	S16710	S16709	T24448
75 2	375 2	176 1	1 94	176 2	176 2	176 2	176 2	176 2	176 2	176 2	176 2	176 2
	100.0											
81	81	81	81	81	81	81	81	81	81	81	81	81
30	33 33	8 E	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1

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C;Accession: 139393
R;Fuchs, E.; Kim, K.H.; Hanukoglu, I.; Tanese, N.
Curr. Probl. Dermatol. 11, 27-44, 1983
A;Title: The evolution and complexity of the genes encoding the cytoskeletal proteins of A;Reference number: 139393; MUID:84083477; PMID:6686106
A;Accession: 139393
                                                                                                                                                                                                                                                                                                                                                                                        A,Molecule type: mRNA
A,Residues: 1-71 <RES>
A,Cross-references: UNIPROT:Q9UE89; GB:M28424; NID:g178023; PIDN:AAB16906.1; PID:g178024
C,Superfamily: actin
                                C.Species: Homo sapiens (man)
C.Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                               A, Status: preliminary; translated from GB/EMBL/DDBJ
lpha-actin - human (fragment)
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Score 81; DB 2; Length 71; Pred. No. 7.8e-07; 100.0%; ilarity 100.0%; Conservative 0 Query Match Best Local Similarity Matches 15; Conserv

Gaps ö 0; Indels Mismatches ;

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1 GGTTMYPGIADRMOK 15 GGTTMYPGIADRMQK 54

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actin - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S14851
R;Burn, T.C.; Tobin, S.L.
R;Burn, T.C.; Tobin, S.L.
A;Reference number: S14851

A;Molecule type: DNA A;Residues: 1-100 <BUR> A;Cross-references: UNIPROT:P02572; EMBL:X54848; NID:g7549; PIDN:CAA38618.1; PID:g7550 C;Genetics:

A;Gene: FlyBase:Act42A A;Cross-references: FlyBase:FBgn0000043 C;Superfamily: actin C;Keywords: cell motility; cytoskeleton; microfilament; mitosis; structural protein

Gaps ö Length 100; Query Match
100.0%; Score 81; DB 2; Length 10
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels

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26 GGTTMYPGIADRMQK 40 1 GGTTMYPGIADRMOK 15 g ઠ

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A;Status: translation not shown
A;Molecule type: DNA
Residues: 1-328 <-LIU5
A;Cross-references: UNIPROT:P83751; EMBL:M25013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references: FlyBase: FBgn0000043
                                                       139 GGTTMYPGIADRMOK 153
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          1 GGTTMYPGIADRMQK 15
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C; Superfamily: actin
                                                                                                                                                                                                                                                                                                                                                                                                    A, Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                             A; Accession: A03000
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Matches
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C; Species: Styela clava
C; Species: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C; Accession: A61043
R; Beach, R.L.; Jeffery, W.R.
Dev. Genet. 11, 2-14, 1990
A; Title: Temporal and Special expression of a cytoskeletal actin gene in the ascidian St
A; Accession: A61043
A; Residues: 1-213 * AEBA
A; Residues: 1-213 * AEBA
A; Residues: 1-213 * AEBA
C; Comment: This sequence is expressed in cells undergoing rapid cell division.
C; Superfamily: actin
C; Keywords: cytoskeleton; methylated amino acid; mitosis; structural protein
F; 73/Modified site: 3'-methylhistidine (His) #status predicted
                                                                  C; Accession: A26337
R; Khrestchatisky, M.; Fontes, M.
J. Mol. Biol. 193, 409-412, 1987
J. Title: There is an alpha-actin skeletal muscle-specific gene in a salamander (Pleurode A; Title: There is an alpha-actin skeletal muscle-specific gene in a salamander (Pleurode A; Reference number: A26337; MUID:87254218; PMID:3453122
A; Accession: A26337
A; Molecule type: DNA
A; Residues: 1-125 < KHR>
A; Residues: 1-125 < KHR>
A; Cross-references: UNIPROT:P10994; GB:X05106; NID:g64248; PIDN:CAA28753.1; PID:g64249
C; Superfamily: actin
C; Keywords: muscle; skeletal muscle
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tin, skeletal muscle - Iberian ribbed newt (fragment)
Species: Pleurodeles waltlii (Iberian ribbed newt)
Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   actin beta - pig (fragments)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 07-Oct-1994 #sequence_revision 12-Apr-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Pred. No. 1.4e-06;
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100.0%; Score 81; DE
Best Local Similarity 100.0%; Pred. No. 1.4
Matches 15; Conservative 0; Mismatches
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Best Local Similarity 100.
Matches 15; Conservative
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C;Accession: A03000
F;Yzberg, E.A.; Bond, B.J.; Hershey, N.D.; Mixter, K.S.; Davidson, N.
Cell 24, 107-116, 1981
A;Title: The actin genes of Drosophila: protein coding regions are highly conserved but a
A;Reference number: A03000; MUID:81210174; PMID:6263481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-308 <FYR>
A;Cross-references: UNIPROT:P02572
A;Note: there are 68 unsequenced residues between positions 160 and 161. Partial sequence
A;Note: the authors translated the codon GTT for residue 263 as 11e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ribiu, Z.; Zhu, Z.; Roberg, K.; Faras, A.J.; Guise, K.S.; Kapuscinski, A.R.; Hackett, P.F. Mucleic Acids Res. 17, 5850, 1989
A.Title: The beta-actin gene of carp (Ctenopharyngodon idella).
A.Reference number: SO5430; MUID:89345185; PMID:2762162
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                                                                                                                                                                                                                                                                                                                                                                                        actin 3 - fruit fly (Drosophila melanogaster) (fragments)
C;Species: Drosophila melanogaster
C;Date: 31-Mar_1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             actin beta - grass carp
C.Species: Ctenopharyngodon idella (grass carp)
C.Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004
                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Query Match 100.0%; Score 81; DB 2; Length 213; Best Local Similarity 100.0%; Pred. No. 2.4e-06; Matches 15; Conservative 0; Mismatches 0; Indels
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C;Superfamily: actin
C;Keywords: cytoskeleton; methylated amino acid
F;73/Modified site: 3'-methylhistidine (His) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 81; DB 2; Length 30 Best Local Similarity 100.0%; Pred. No. 3.6e-06; Matches 0; Mismatches 0; Indels
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Local Similarity 100.0%; Pred. No. 3.8e-06,
Nes 15; Conservative 0; Mismatches 0;
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A;Cross-references: GB:K00622; GB:K00623
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  300 GGTTMYPGIADRMOK 314
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Best Local Similarity 100.0
Matches 15, Conservative
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C; Species: Bos primigenius taurus (cattle)
C; Accession: E14185; A39105; Ā02999; A14185
R; Vandekerckhove, J.; Weber, K.
Bur. J. Biochem. 90, 451-462, 1978
A; Title: Actin maino-acid sequences. Comparison of actins from calf thymus, bovine brain A; Reference number: A14185; MUID:79045349; PMID:213279
A; Accession: E14185
A; Molecule type: protein
A; Residues: 1-34 vMA
A; Cross-references: UNIPROT: P60712
A; Note: only peptides that differed in composition from the corresponding peptides of ra
A; Note: only peptides that differed in composition from the corresponding peptides of ra
A; Note: only peptides that differed in mitogen-activated bovine lymphocytes. Analye
A; Riegerence number: A39105; MUID:84032385; PMID:6195151
A; Accession: A39105
A; Molecule type: mRNA
A; Residues: 76-227;344-374 vDEG>
                              actin, fetal skeletal/adult cardiac muscle - mouse (fragment)

C;Species: Mus musculus (house mouse)
C;Date: 23-Aug-1897 #sequence_revision 23-Aug-1987 #text_change 09-Jul-2004
C;Accession: B25819
C;Accession: B25819
C;Accession: B25819
C;Accession: B25819
A;Alonso, S; Minty, A; Bourlet, Y; Buckingham, M.
A;Alonso, S; Minty, A; Bourlet, Y; Buckingham, M.
A;Alonso, S; Minty, A; Bourlet, Y; Buckingham, M.
A;Reference number: A25819; MUD:86200234; PMID:3084797
A;Accession: B25819
A;Ac
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C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 09-Sep-1987 #sequence_revision 09-Sep-1987 #text_change 05-Dec-1997
C;Accession: A26559
R;Bergsma, D.J; Chang, K.S.; Schwartz, R.J.
Mol. Cell. Biol. 5, 1151-1162, 1985
A;Accession: A26559; MUID:85213487; PMID:4000121
A;Accession: A26559
A;Molecule type: DNA
A;Residues: 1-362 - kBER>
C;Superfamily: actin
C;Keywords: cytosol; methylated amino acid
F;74/Modified site: 3'-methylhistidine (Hi8) #status predicted
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100.0%; Pred. No. 4.1e-06;
...ve. 0; Mismatches -0; Indels
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Matches 15; Conserv
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C; Superfamily: actin
K; Meywords: blocked amino end; cell motility; cytoskeleton; methylated amino acid; micro
F;1/Modified site: blocked amino end (Asp) (probably acetylated) #status experimental
F;72/Modified site: 3'-methylhistidine (His) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R. Vandekerckhove, J.; Weber, K. St. St. J. St. M. St. J. St. M. St. J. 
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C;Keywords: blocked amino end; cell motility; cytoskeleton; methylated amino acid; micro
F;J/Modified site: blocked amino end (Glu) (probably acetylated) #status experimental
F;72/Modified site: 3'-methylhistidine (His) #status predicted
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C.Species: Homo eaplens (man)
C.Species: Homo eaplens
C.Species: Homo ea
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A;Residues: 1-374 <VAN>
A;Cross-references: UNIPROT:P02571
A;Note: only peptides that differed in composition from the corresponding peptides of reC;Comment: Vertebrate nonmuscle cells contain two highly conserved cytoskeletal actins,
A;Note: actins beta and gamma were not distinguished in this study
C;Comment: Vertebrate nonmuscle cells contain two highly conserved cytoskeletal actins,
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A;Residues: 1-61;84-112;147-190;196-209;215-253;335-358 <HA2>
A;Residues: 1-61;84-112;147-190;196-209;215-253;335-358 <HA2>
A;Residues: 1-61;84-112;147-190;196
C;Comment: This protein is involved in a signal transduction that eventually leads to C;Superfamily: actin
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C;Date: 30-Sep-1991 #segnee_revision 30-Sep-1991 #text_change 09-Jul-2004
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No. 4.4e-06; Matches 15; Conservative 0; Mismatches 0; Indels
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100.0%; Score 81; DB 1; Length 37
Best Local Similarity 100.0%; Pred. No. 4.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels
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A;Title: A novel 27/16 kDa form of subtilisin cleaved actin: structural and functional coa; Reference number: 865873; MUID:95300963; PMID:7781768
A;Accession: 865873
                                                                                                                 A;Molecule type: protein
Ms.Residues: 235-241 < VAH.
R;Residues: 235-241 < VAH.
R;Strzelecka-Golaszewska, H.; Wozniak, A.; Hult, T.; Lindberg, U.
Biochem. J. 316, 713-721, 1996
Biochem. J. 316, 713-721, 1996
A;Title: Effects of the type of divalent cation, Ca2+ or Mg2+, bound at the high-affinity
A;Reference number: S70610; MUID:96265033; PMID:8670143
A;Accession: S70610
                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: protein
A;Meaidues: 48-54;68-72:35-243 <STR>
A;Reaidues: 48-54;68-72:435-243 <STR>
A;Reaidues: 48-54;68-72:425-243 <STR>
A;Experimental source: seeletal muscle
R;Bertrand, R.; Dexancourt, J.; Kassab, R.
R;Bertrand, R.; Ja-119; J. 1994
A;Bertrand, R.; Ja-119; J. 1994
A;Title: The covalent maleimidobenzoyl-actin-myosin head complex. Cross-linking of the 50;A;Reference number: S44393; MUID:94259162; PMID:8200441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           methylated amino acid; muscle contraction
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A; Mesidues: 1-375 < NUD.
A; Ctross-references: GB:J00691; NID:g202653; PIDN:AAA40657.1; PID:g202654
C; Comment: Vertebrate nonmuscle cells contain two highly conserved cytoskeletal actins,
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C;Reymords: cell motility; oytoskeleton; methylated amino acid; microfilament; mitosis;
E;2-375/Product: actin beta #status predicted <MAT>
F;73/Modified site: 3'-methylhistidine (His) #status predicted
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C;Date: 13-Jun-1983 #sequence_revision 13-Jun-1983 #text_change 22-Jun-1999
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R;Nudel, U.; Zakut, R.; Shani, M.; Neuman, S.; Levy, Z.; Yaffe, D.
Nucleic Acids Res. 11, 1759-1771, 1983
A;Title: The nucleotide sequence of the rat cytoplasmic beta-actin gene.
A;Reference number: A38571; WUID:83168920; PMID:6300777
A;Accession: A38571
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F:1/Modified site: acetylated amino end (Asp) #status experimental F:73/Modified site: 3'-methylhistidine (His) #status experimental
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100.0%; Pred. No. 4.4e-06;
iive 0; Mismatches 0;
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A;Residues: 48-64 <BER>
Experimental source: skeletal muscle
C;Superfamily: actin
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Conservative 0;
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Best Local Similarity
Matches 15; Conserv
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les 15; Conserv
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C,Bate: 30-Sep-1991 #sequence revision 30-Sep-1991 #text change 07-May-1999
C;Bate: 30-Sep-1991 #sequence revision 30-Sep-1991 #text change 07-May-1999
C;Bate: 30-Sep-1991 #sequence revision 30-Sep-1991 #text change 07-May-1999
C;Accession: A5182; A14185; $55873; $70610; $44393; A02994
R;Collins, J.H.; Elzinga, M.
J. Biol. Chem. 250, 5915-5920, 1975
A;Title: The primary structure of actin from rabbit skeletal muscle. Completion and anal A;Reference number: A2182; MUID:75211334; PMID:1150665
A;Molecule type: protein
A;Residues: 1-2, TT, 4, D', 6-11, 'D', 13-73, 'W', 74-78, 80-234, 236-308, 'T', 310-375 <COL>
A;Molecule type: protein
A;Residues: 1-2, 'TT, 4, D', 4-10', 6-11, 'D', 13-73, 'W', 74-78, 80-234, 236-308, 'T', 310-375 <COL>
A;Molecule type: protein
A;Residues: 09, 43-1462, 1978
A;Molecule type: group as been revised in references A14185 and A90406
A;Molecule type: protein
A;Reference number: A14185; MUID:79045349; PMID:213279
A;Molecule type: protein
A;Reference number: A14185; MUID:78060866; PMID:588555
A;Molecule type: protein
A;Reference number: A90406; MUID:78060866; PMID:588555
A;Molecule type: protein
A;Reference number: A90406; MUID:78060866; PMID:588555
A;Molecule type: protein
A;Reference number: amnotation
A;Molecule type: protein
A;Molecule type: p
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A; Accession: A02997
A; Accession: A02997
A; Modified site: 30.2000
A; Accession: A02997
A; Modified site: A135 < VAN>
A; Residues: 1-375 < VAN>
B; Zevgolis, V.G.; Sotiroudis, T.G.; Evangelopoulos, A.E.
Biochim. Biophys: Acta 1091, 222-230, 1991
A; Title: Phosphorylase kinase from bovine stomach smooth muscle: a Ca(2+)-dependent prot A; Reference number: S13480; MUID:91137633; PMID:1995080
A; Molecule type: protein
A; Residues: 40-49 < ZEV>
A; Residues: 40-49 < ZEV>
A; Experimental source: stomach
A; Note: this material appears to be actin of acrtic smooth muscle type or a related mole C; Superfamily: actin
C; Keywords: acetylated amino end; methylated amino acid; muscle contraction
F; 1/Modified site: acetylated amino end (Glu) #status predicted
F; 73/Modified site: 3'-methylhistidine (His) #status experimental
                                                                                                                                                                                                                                                                                                                                                                           C,Accession: A02997; Moder, K.
R,Vandekerckhove, J.; Weber, K.
Pfifferentiation 14, 123-133, 1979
A;Title: The complete amino acid sequence of actins from bovine aorta, bovine heart, bovitation.
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                                                                                                                                                                                                                                                                                                      Species: 80s primigenius taurus (cattle)
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100.0%; Pred. No. 4.4e-06;
tive 0; Mismatches 0; Indels
                                                                    300 GGTTMYPGIADRMOK 314
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Best Local Similarity 100.0
Matches 15; Conservative
                                                                                                                                                                                                                                                                          actin, aortic smooth muscle
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us-09-423-351c-4.rup

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apis cerana
marmota mon
anguilla ja
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diadromus p
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anàs platyr
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boophilus m
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                                                       April 8, 2005, 09:58:56; Search time 57.8667 Seconds (without alignments) 132.739 Million cell updates/sec
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                  1612378 segs, 512079187 residues
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Maximum Match 100%
Listing first 45 summaries
                                     - protein search, using sw model
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Q7ZZZQ
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Q8UA7
Q8J1Q2
P91881
O76493
Q6R127
Q6R128
Q6R128
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Gapop 10.0 , Gapext 0.5
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1 GGTTMYPGIADRMQK 15
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2: uniprot_trembl:*
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Q6ptc2 sitobion av Q66del homo sapien Q96del homo sapien Q96fue homo sapien Q96fue homo sapien Q96fue chironomus Q6gxe6 lepisosteus Q7xx59 rana catesb Q86cv5 drosophila Q66xj3 drosophila Q6xj3 drosophila Q9ygy6 oreochromis Q7m3b0 sus scrofa Q6sq19 helcion pel Q7m3y7 styela clav	NTS 60 AA. ace update) ation update) ; Vertebrata; Euteleostomi; dia; Canidae; Canis.	PubMed=8855304; DOI=10.1073/pnas.93.20.11035; S., Lee M.A., Lindpaintner K.; systemic factors, regulate gene expression of the otensin system in vivo: a comprehensive study of all the dog."; Sci. U.S.A. 93:11035-11040(1996). Sci. U.S.A. 93:11035-11040(1996). Sci. u.S.A. 93:11035-11040(1996). Actin_like. 1. 1. 1. 60 6744 MW; AA02DE065D32D7C4 CRC64;	; DB 2; Length 60; . 5e-06; ches 0; Indels 0; Gaps 0;	71 AA. nce update) ation update) , Vertebrata; Buteleostomi; ni; Hominidae; Homo.
Q6 PTC2 Q9 G6 BE1 Q9 G6 BE1 Q9 G GR4 Q6 GGX E Q7 GGX E Q6 GCV S Q6 GCV S Q6 GGY E Q6 GGY E Q6 GGY E Q6 GGY E Q6 GGY E Q6 GGY E	ALIGNMENTS PRT; 60 A Created) Last sequence Last annotatio a; Craniata; Ve ra; Fissipedia;	SEQUENCE FROM N.A. MEDLINE=97008128; PubMed=8855304; DOI=10.1(Lee Y.A., Liang C.S., Lee M.A., Lindpaintne "Local stress, not systemic factors, regula cardiac renin-angiotensin system in vivo: a its components in the dog."; Proc. Natl. Acad. Sci. U.S.A. 93:11035-1104 ENBL; PO2568; LMA9. GO; GO:0015629; C:actin cytoskeleton; IEA. GO; GO:0015629; C:actin cytoskeleton; IEA. GO; GO:002500; F:structural constituent of InterPro; PRR04000; Actin_like. Pfam; PP00022; Actin; 1. NON_TER 1 1 1 1 1 1 1 1 1 1 1 1 1	; Score 81; ; Pred. No. 5 0; Mismatche	PRT; 71 A Created) Last sequence Last annotatio a; Craniata; Ve s; Catarrhini;
0000000000000000	02, 02, 24, dat	MW;	.0. .0. 115	113, 24, adat
149 159 1659 171 171 171 181 183 183 203	PRELIMINARY; (TrEMBLrel. 02, Ca (TrEMBLrel. 02, La (TrEMBLrel. 24, La Fragment). aris (Dog). letazoa; Chordata;	Pubmed=881. S., Lee M. S., Lee M. iotensin s) the dog." Sci. U.S. 48640.1; 9. actin cyte. sartin cyte. sartin cyte. sartin cyte. 100; Actin. 11.	100.0%; imilarity 100.0%; ; Conservative 0 GGTTMYPGIADRWQK 15 GGTTMYPGIADRWQK 34	PRELIMINARY; (TrEMBLrel. 13, C (TrEMBLrel. 24, I (TrEMBLrel. 24, I (Trement). Fragment). Fragment). Fragment). Fragment). Fragment). Fragment). Fragment). Fragment). Fragment). Fragment (Trement). Fragment). Fragment (Trement). Fragment (Trement)
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	LT 1 64 095164 095164; 00-FEB-1997 01-FEB-1997 01-TM-2003 Beta-actin (Canis famili Eukaryota; Mammalia; Eu	SEQUENCE FROM N.A. MEDLINE=97008128; Pub Lee Y.A., Liang C.S., "Local stress, not sy cardiac renin-angiote its components in the Proc. Natl. Acad. Sci EMBL; UG7202; AAC4864 HSSP; P02568; 1MA9. GO; GO:0015629; C:act GO; GO:0015629; C:act GO; GO:0005200; F:str InterPro; IPR004000; Pfam; PF00022; Actin; NON TER 1 6 SEQUENCE 60 AA; 67	atch cal S 15 1	39 39; 4Y-20 IN-20 IN-20 Sapi Fyota alia; Taxi ITaxi
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Gaps
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Actinopterygii, Neopterygii, Teleostei, Euteleostei, Neoteleostei, Acanthomorpha, Acanthopterygii, Percomorpha, Atherinomorpha, Cyprinodontiformes; Fundulidae, Fundulus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-92249656; PubMed-1577198;
Beach K.L., Jeffery W.R.,
Beach K.L., Jeffery W.R.,
"Multiple actin genes encoding the same alpha-muscle isoform are expressed during ascidian development.";
bev. Biol. 15:155-66(1992).
EMBL, L13788; AAA29846.1;
HSSP; P02568; 1QZS.
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                                                                                                                                                                                                                              GO; GO:0005884, C:actin filament; IEA.
GO; GO:0003774; F:motor activity; IEA.
GO; GO:0002020; F:structural constituent of cytoskeleton; IEA.
PEROSITE; PSO0432; ACTINS_2; 1.
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GO; GO:0003774; F:motor activity; IEA.
GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
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Pred. No. 8.4e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                          Score 81; DB 2; Length 96;
Pred. No. 8.1e-06;
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                                                                                                                                                Roling J.A., Baldwin W.S.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF435092; AAL29465.1; -.
HSSP: P02568; 1025.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chordata; Urochordata; Ascidiacea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100 AA; 11264 MW; 108CE34548BABB5E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                  96 AA; 10798 MW; 7440DA6AE5A070C4 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Stolidobranchia, Styelidae, Styela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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InterPro; IPR004000; Actin_like.
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PROSITE; PS00432; ACTINS 2; 1;
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Best Local Similarity 100.
Matches 15; Conservative
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les 15; Conserv
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                                                                 NCBI_TaxID=8078;
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                                                                                                                              rissum=Liver;
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                   Fuchs E., Kim K.H., Hanukoglu I., Tanese N.; "The evolution and complexity of the genes encoding the cytoskeletal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Q90X51;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Beta-actin (Fragment).
Fundulus heteroclitus (Killifish) (Mummichog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anas platyrhynchos (Domestic duck).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
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0
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GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
InterPro; IPR0040404 Actin_like.
Pfam; PF00022; Actin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0005884; C.actin filament; IEA.
GO; GO:0003774; F:motor activity; IEA.
GO; GO:0003709; F:motorial constituent of cytoskeleton; IEA.
InterPro; IPR004000; Actin_like.
                                                                                                                                                                                                                                                                                                                                       100.0%; Score 81; DB 2; Length 71; 100.0%; Pred. No. 5.9e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 81; DB 2; Length 93;
Pred. No. 7.8e-06;
                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Spleen;
Sreekumar E., Premraj A., Rasool T.J.;
Submitred (MAR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AY251-75; AAP04479.1;
HSSP; P02569; 1025.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93 AA; 10444 MW; F867ADF144D80523 CRC64;
                                                                                                                                                                                                                                                                        71 71 71 71 71 AA; 7799 MW; D3886403C855CF70 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93 AA
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                                                        proteins of human epidermal cells.";
Curr. Probl. Dermatol. 11:27-44(1983).
EMBL, MX8424, AAB16906.1; -.
PIR; 139393; 139393.
HSSP; P02568; 1MA9.
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PROSITE; PS00432; ACTINS_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                        1 GGTTMYPGIADRMQK 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19 GGTTMYPGIADRMQK 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                             40 GGTTMYPGIADRMOK 54
                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 15; Conservative
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1es 15; Conservative
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01-MAR-2004 (TrEMBLre
Beta-actin (Fragment)
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07ZZZ0;
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Anguilla japonica (Japanese eel).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Anguilliformes, Anguillidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Hymenoptera, Tenthredinoidea, Diprionidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO; GO:0015629; C:actin cytoskeleton; IEA.
GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
InterPro; IPR004000; Actin_like.
Pfam; PF00022; Actin; 1.
NON TER 107 107
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GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
InterPro; IPR004000; Actin_like.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 81; DB 2; Length 107; 100.0%; Pred. No. 9e-06; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 81; DB 2; Length 109;
                                                                                                                                                                                                                                                                                                                                                                                    Kurokawa T.;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; ABD74846; BAB96533.1; -.
HSSP; P10983; 1D4X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bigot Y.B.;
Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               107 AA; 12006 MW; 375A7A5C6E6CEA3A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          109 AA; 12036 MW; 15F3926BBD263554 CRC64;
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                  Last sequence update)
Last annotation update)
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                                                                                            107 AA
                                                                                                                                  Created)
                                                                                            PRT;
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                                                                                        08J102
08J102;
08J102;
01-OCT-2002 (TrEMBLrel. 22, Cr
01-OCT-2002 (TrEMBLrel. 22, Le
01-JUN-2003 (TrEMBLrel. 24, Le
Beta-actin (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X91507; CAA62807.1; -. HSSP; P10983; 1D4X.
32 GGTTMYPGIADRMQK 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GGTTMYPGIADRMQK 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81
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Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67 GGTTMYPGIADRMQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00022; Actin; 1.
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                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Pancreas;
                                                                                                                                                                                                                                                                                                        NCBI_TaxID=7937;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Diprion pini
                                                                                                                                                                                                              Name=b-act;
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P91877
                                                        RESULT 8
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EMBL; AXI70121; AAO39434.1; -.
                                                                                                                                                                                                                              Shimizu I., Kawai Y., Taniguchi M., Aoki S.,
"Circadian rhythm and cDNA cloning of the clock gene period in the honeybee Apis cerana japonica.";
Zool. Sci. 18:779-789(2001).
EMBL; ABO72495; BAB69483.1; -.
HSSP; P10983; 1D4X.
                                                                                          Apis cerana (Indian honeybee).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Sciuridae, Sciurinae,
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GO; GO:0003774; F:motor activity; IEA.
GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
InterPro; IPR004000; Actin_like.
                                                                                                                                                                                                                                                                                                                                            GO; GO:0015629; C:actin cytoskeleton; IEA.
GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
InterPro: IPRO04000; Actin_like.
Pfam; PF00022; Actin, 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 103;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                5203DA3630FCD807 CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                  01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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100.0%; Pred. No. 8.7e-06;
tive 0; Mismatches 0;
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                    01-DEC-2001 (TrEMBLrel. 19, Created)
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PROSITE; PS00432; ACTINS_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              103 AA; 11520 MW;
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01-MAR-2004 (TrEMBLrel. 2-
Beta-actin (Fragment).
Marmota monax (Woodchuck)
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Best Local Similarity 100.
Matches 15; Conservative
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                                                                                                                                                                    NCBI_TaxID=7461;
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                                                                          Actin (Fragment)
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Q80UA7 RESULT 7 Q80UA7

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Length 110;

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110 AA; 12070 MW; DD2831BC3D4D3EF8 CRC64;
                           100.0%; Score 81; DB 2; I 100.0%; Pred. No. 9.3e-06;
                                                                                1 GGTTMYPGIADRMQK 15
                                                                                               GGTTMYPGIADRMQK 89
                                                     15; Conservative
                                                                                                                                                                        PRELIMINARY;
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Best Local Similarity
                                       Sest Local Similarity
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Q6R128
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                Gaps
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Bemisia argentifolii (silverleaf whitefly).

Bukaryota, Metazoa; Arthropoda; Haxapoda; Insecta; Pterygota;

Neoptera; Parameoptera; Hemiptera; Sternorrhyncha; Aleyrodiformes;

Aleyrodoidea; Aleyrodidae; Aleyrodinae; Bemisia.
                                                                                                                                                                                                         Diadromus pulchellus (Parasitic wasp).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Hymenoptera; Apocrita; Ichneumonidea;
Ichneumonidae; Ichneumoninae; Diadromus.
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                                                                                                                                                                                                                                                                                                  Hamelin E., Bigot Y.Y.B., Rouleux F., Renault S., Periquet G., Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
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GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
InterPro; IPR004000; Actin_like.
Pfam: PF00022; Actin_like.
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GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
InterPro; IPR004000; Actin_like.
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             Indels
                                                                                                                                                                                                                                                                                                                                                       Bigot Y.B.;
Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.
EMBL: X91506; CAA62806.1; -.
HSSP; P10983; 1D4X.
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He M., Haymer D.S., Lai P.Y.;
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF071998; AAC24152.1;
HSSP; P10983; 1D4X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   109 AA; 12251 MW; 3C34D292C5AA039A CRC64;
                                                                                                                                                     01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
100.0%; Pred. No. 9.2e-06;
tive 0; Mismatches 0;
                                                                                                                                 109 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 110 AA
                                                                                                                                 PRT;
                                       1 GGTTMYPGIADRMOK 15
                                                              54 GGTTMÝPGIADRMOK 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GGTTMYPGIADRMOK 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54 GGTTMYPGIADRMQK 68
Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00022; Actin; 1.
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                                                                                                                                                                                                                                                               NCBI_TaxID=7420;
                                                                                                                                                                                            Actin (Fragment)
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01-JUN-2003
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SEQUENCE
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P91881;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (Tremment).
Boophilus microplus (Cattle tick).
Buophilus microplus (Cattle tick).
Bukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
Parasitiformes; Ixodida; Ixodidae; Boophilus.
                06R127;
06-UUL-2004 (TYEMBLrel. 27, Created)
05-UUL-2004 (TYEMBLrel. 27, Last sequence update)
05-UUL-2004 (TYEMBLREL. 27, Last annotation update)
Beta-actin (Fragment).
Boophilus microplus (Cattle tick).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 81, DB 2; Length 111; Pred. No. 9.4e-06; O; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Holmes S.P., Barron P.D., He H., Pietrantonio P.V.;
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AYS19366; AAS09967.1; -
                                                                                                                                                                                                                                                                       Holmes S.P., Barron P.D., He H., Pietrantonio P.V.;
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AYS19367; AAS09968.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    111 111
111 AA; 12294 MW; 40F58D31A43B48F5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                           111 AA; 12310 MW; 5639572768E148F5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 81; DB 2; L 100.0%; Pred. No. 9.4e-06;
111 AA.
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Best Local Similarity 100.0
Matches 15, Conservative
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                                                                                                                             Alpha-actin protein (Fragi, Library and Pagrus again, Pagrus major (Red sea bream) (Chrysophrys major).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Sparitomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidei;
Sparidae; Pagrus.

NCBI_TaxID=143350;
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Scyliorhinus torazame (Cloudy catshark).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Blasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
Scyliorhinidae; Scyliorhinus.
NCBI_TAXID=75743;
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Kim J.T., Kim M.S., Jang B.R., Kim Y.J., Kim K.W.;
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF305690; AAG22088.1;
HSSP; P02568; 1QZ5.
GO; GO:0015629; C:actin cytoskeleton; IEA.
GO; GO:0015000; F:structural constituent of cytoskeleton; IEA.
InterPro; IPR004000; Actin_like.
PF00022; Actin; 1.
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Chen S.L., Xu M.Y., Hu S.L., Li L.;
"Analysis of immune-relevant genes expressed in red sea bream
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, AY190676, AAP20152.1; -
GO: GO:000584; C:actin filamet; IEA.
GO: GO:0003774; F:mctor activity: IEA.
GO: GO:0005200; F:structural constituent of cytoskeleton; IEA.
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Pred. No. 9.5e-06;
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                                                  05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
  113 AA
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SEQUENCE
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Search completed: April 8, 2005, 12:03:08 Job time : 59.8667 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

; Search time 62.4 Seconds (without alignments) 92.971 Million cell updates/sec April 8, 2005, 09:58:56 Run on:

US-09-423-351C-5 81 1 PRHQGVMVGMGQKDS 15 Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 segs, 386760381 residues Searched:

Total number of hits satisfying chosen parameters:

2105692

seq length: 0 seq length: 200000000 Minimum DB E Maximum DB E Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp2002s:* A_Geneseq_16Dec04:* 1: genesedro19A0a.* geneseqp2003as:*geneseqp2003bs:*geneseqp2004s:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

	Description	Aaw92531 Beta-acti	Abp42469 Human ova	Abb66853 Drosophil	Abp43176 Human ova		Abg15288 Novel hum	Abo58422 Human gen	Adr38362 pigA3Cy3G	~	Aay78101 Misgurnus		Aap61532 Sequence	Aar50328 Drug resi	Aab15017 Posttrans	Aay94569 Human car	Aab15016 Posttrans	Abb77395 Human act	Н	Abm04830 Rat cytop	Adb85212 Rat actin	Ade61174 Rat Prote	Adf30525 Rat angio	Adi63062 Human apo	Adi62970 Human apo	Adi63040 Human apo
	ID	AAW92531	ABP42469	ABB66853	ABP43176	ABP43016	ABG15288	AB058422	ADR38362	ADM05323	AAY78101	AAB12985	AAP61532	AAR50328	AAB15017	AAY94569	AAB15016	ABB77395	ABR64271	ABM04830	ADB85212	ADE61174	ADF30525	ADI 63062	ADI62970	AD163040
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ADL13002 ADJ78489	ADP04899 ADP12391	ADQ26098 ABO84772	ABM80841 ADN23274	ADS88828 ADS88825	ADS88826	ADS88827 AAW19799	ABB58162	ABB61322 ABB60354	ABB64853	ABR62327	ADN03845
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26	3 7 8 3 7 8 3 7 8	31 32	33 34	36 36	37	3 8 3 8	40	4 4 1 2	43	44	45

## ALIGNMENTS

Peptide substrate; CCT; eukaryotic type II chaperonin complex; cyclin; binding agent; substrate-binding site; SBS; substrate folding; actin; tubulin; treatment; cancer; anticancer drug; viral infection; screening; Beta-actin reference peptide substrate #5. AAW92531 standard; peptide; 15 AA (first entry) reduced toxicity. 26-APR-1999 AAW92531; RESULT 1 AAW92531 

Synthetic.

WO9853322-A1

26-NOV-1998.

98WO-GB001485. 22-MAY-1998; 97GB-00010762. 23-MAY-1997; (CANC-) INST CANCER RES ROYAL CANCER HOSPITAL.

Liou AK; Willison K, Hynes G,

WPI; 1999-070162/06.

Identifying specific binding agents for substrate binding site in CCT chaperonin complex - also new peptide binding agents and their mimetics, and peptides containing a specific CCT binding site, used for treating cancer.

Disclosure, Fig 10; 97pp; English.

This invention describes a method which uses the CCT (eukaryotic type II chaperonin) complex or part of it, for identifying a binding agent that can occupy a substrate-binding site (SBS) on the CCT complex. By binding agents block an SBS so that biological activity of the CCT complex is affected, particularly its ability to fold substrates such as actin, tubulin and cyclin. The binding agents are useful for treatment of cancer, particularly when used in combination with an anticancer drug, or viral infections. Nucleic acid fragments are used to screen for agents, e.g. binding agents that modulate interaction between the CCT complex and a protein that is to be folded. The binding

toxoplasmosis, and toxic

infections (e.g., chlamydia, HIV,

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RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and neurological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also encompasses polypeptides 90% identical and polynucleotides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigen polynucleotides, antibodies against human ovarian antigens of ovarian antigens polynucleotides, antibodies and polypeptides in diagnosing, treating, prognosing or preventing various ovary and/or breast-related disorders. Such condittions include ovarian cancer and breast cancer, and metastatic tumours of ovarian or breast origin, reproductive system disorders (e.g., infertility, disorders of pregnancy, anovulation, polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndrome; PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection; inflammatory condftion; immune disorder; blood disorder; respiratory disorder; neurological disorder; cardiovascular disorder; respiratory disorder; neurological disorder; gene therapy; chromosome mapping; forensic analysis; antibody preparation; cytostatic; immunomodulatory; neuroprotective; antibiliammatory; gynaecological; reproductive.
                         80
gents may target cells that are actively synthesising tubulin etc. (unlike known microtubule-stabilising agents that affect all cells), should have reduced toxicity for normal cells. AAW92527-W92541 are
                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                         ovarian antigen; ovary; ovarian; breast; cancer; tumour;
                                                                                                                         Length 15
                                                                                                                                                    0; Indels
                                                     peptide substrates used in the method of the invention
                                                                                                                     Score 81; DB 2; I
Pred. No. 2.8e-07;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                     ABP42469 standard; protein; 105 AA.
                                                                                                                       100.0%;
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                                                                                      Sequence 15 AA;
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wagnitis), inflammatory conditions (e.g., mastitis, comportis and vagnitis), immune disorders (e.g., congenital and acquired vagnitis), immune disorders (e.g., congenital and acquired immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus), blood-related disorders (e.g., anaemia), cardiovascular disorders), respiratory disorders, neurological disorders, gastrointestinal disorders and isorders. Ovarian antigen polypeptides and polypucleotides may also be used in screening for compounds which modulate ovarian antigen or activity. The polynucleotides may further be used for gene therapy, chromosome mapping, in the collipse of individuals and in forensic analysis, and the polypeptides may be used as food additives or to prepare antibodies useful in disease diagnosis, drug targeting and phenotyping. The present sequence represents a human ovarian antigen of the invention. Note: The sequence data for this patent did not form part of the printed sequence data for this patent did not form part of the printed sequence in the collection of the collection of the printed sequence are collective to the printed sequence data for this patent did not form part of the printed sequence are collective to the printed to the prin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 81; DB 5; Length 105; 100.0%; Pred. No. 2.2e-06; ive 0; Mismatches 0; Indels
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11-JUL-2000; 2000US-00614150.
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Best Local Similarity
'-haq 15; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB66853;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP41228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also encompasses polypeptides 90% identical and polymucleotides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigen polymucleotides, antibodies against human ovarian antigens of ovarian antigens polymucleotides and polypeptides in diagnosing, treating, prognosing or preventing various ovary and/or breast-related disorders. Such conditions include ovarian cancer and breast cancer, and metastatic tumours of ovarian or breast origin, reproductive system disorders (e.g., infertility, disorders of pregnancy, anovulation, polycystic ovary syndrome, ovarian cystes, and dysmenorrhoea), endocrine disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ovarian cancer, breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndrome; PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection; inflammatory condition; immume disorder; blood disorder; infection; cardiovascular disorder; respiratory disorder; neurological disorder; gens trointestinal disorder; urinary system disorder; drug screening; gene therapy; chromosome mapping; forensic analysis; antibody preparation; cytostatic; immunomodulatory; neuroprotective; antiinflammatory; synaecological; reproductive.
                    printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
patent did not form part of the
                                                                                                                                                           Gaps
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                                                                                                                    Length 157;
                                                                                                                                                     0; Indels
                                                                                                                    Score 81; DB 4; I
Pred. No. 3.5e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human ovarian antigen HVVCQ49, SEQ ID NO:4308.
                                                                                                                                                           Mismatches
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  ABB72072). The sequence data for this
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100.0%;
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                                                                                                                                                                                                1 PRHQGVMVGMGQKDS 15
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                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                  Query Match 100.
Best Local Similarity 100.
Matches 15; Conservative
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                                                                               Sequence 157 AA;
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cuagnitis), inmune disorders (e.g., congenital and acquired the vaginitis), immune disorders (e.g., congenital and acquired the vaginitis), immune disorders (e.g., congenital and acquired the conformation of immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus), blood-related disorders (e.g., anaemia), cardiovascular disorders, blood-related disorders (e.g., anaemia), cardiovascular disorders (c.g., anaemia), cardiovascular disorders and urinary system disorders. Ovarian antigen polypeptides and polymucleotides may also be used in screening for compounds which modulate ovarian antigen expression or activity. The polymucleotides may further be used for gene therapy, chromosome mapping, in the identification of individuals and in forensic analysis, and the collections and prepare antibodies useful in disease diagnosis, drug targeting and phenotyping. The present sequence represents a human ovarian antigen of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                              Length 201;
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100.0%; Pred. No. 4.5e-06;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human ovarian antigen HSPSB24, SEQ ID NO:4148.
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                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.8
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                      Sequence 201 AA;
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The invention trained to 2175 Hover numen ovarian antigens (ABP41228) and to coDRAs encoding them (ABO64131-ABO6505), and also encompasses polypeptides 90% identical and polynucleotides 95% identical to the thrention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigen polynucleotides against human ovarian antigens, and the use of ovarian integens ovary and/or breast related disorders. Such conditions include ovarian cancer and breast cancer, and metastric tunnours of ovarian or breast origin, reproductive system disorders (e.g., infertinity, disorders of pregnancy, anovulation, polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine disorders, infections (e.g., chlamydia, HIV, toxoplamenosis, and toxic shock syndrome), inflammatory conditions (e.g., congenital and acquired therefores, infections (e.g., congenital and acquired toxoplamentories, autoimmune ophorities, systemic lupus erythematosus, chood-related disorders (e.g., anaemia), cardiovascular disorders, blood-related disorders (e.g., anaemia), cardiovascular disorders (blood-related disorders, neurological disorders, gastrointestinal disorders of polymulate ovarian antigen expression or activity. The polymucleotides may also be used in screening for compounds which modulate ovarian antigen expression or activity. The polymucleotides may be used as food additives or to prepare antibodies (e.g., pushing in disease diagnosis, drug targeting and phenotyphing. The present sequence represents a human ovarian antigen of the invention. Note: The squence data for this patent did not form part of the printed sequence data for this patent did not form part of the printed sequence data for this patent did not form part of the printed of the prin
   invention relates to 2175 novel human ovarian antiqens (ABP41054-
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ö Gaps ; 100.0%; Score 81; DB 5; Length 204; 0; Indels Pred. No. 4.6e-06; 100.0%; Prec. ... Best Local Similarity 100. Matches 15; Conservative Query Match

1 PRHQGVMVGMGQKDS 15 58 PRHOGVMVGMGOKDS 72 ð 셤

ABG15288 standard; protein; 207 AA. ABG15288; ABG15286 

Novel human diagnostic protein #15279 18-FEB-2002 (first entry)

Human; chromosome mapping; gene mapping; gene therapy; forensic food supplement; medical imaging; diagnostic; genetic disorder

Homo sapiens.

WO200175067-A2.

11-OCT-2001.

30-MAR-2001; 2001WO-US008631

2000US-00540217 23-AUG-2000; 2000US-00649167 31-MAR-2000;

(HYSE-) HYSEQ INC.

Drmanac RT,' Liu C,

Tang YT;

WPI; 2001-639362/73. N-PSDB; AAS79475 New isolated polynucleotide and encoded polypeptides, useful in

New human genome-derived single exon nucleic acid probes useful for human gene expression analysis, for identifying or characterizing alternative splicing events, for assessing genomic alterations or as tools for

Hanzel DK;

Rank DR,

Penn SG,

WPI; 2004-119264/12.

The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed cativity of (II) as useful in gene therapy techniques to restore normal activity of (II) to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in issue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders of sites expressing (II), (I) and (II) are useful for treating disorders of polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic maino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in parent did not appear in the printed specification, but was obtained in Gaps diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity. .. 0 Length 207; Indels Human; gene expression; single exon probe; microarray; alternative splicing event; genomic alteration. 100.0%; Score 81; DB 4; I 100.0%; Pred. No. 4.7e-06; Human genome derived single exon protein #4656. Mismatches Claim 20; SEQ ID NO 45647; 103pp; English. ftp.wipo.int/pub/published pct_sequences ABO58422 standard; protein; 219 AA. ó, 03-APR-2002; 2002US-00029386. 03-APR-2002; 2002US-00029386. 1 PRHOGVMVGMGOKDS 15 PRHOGVMVGMGOKDS 79 (first entry) Conservative (PENN/) PENN S G. (RANK/) RANK D R. (HANZ/) HANZEL D K. Local Similarity nes 15; Conserv Sequence 207 AA; US2003194704-A1. Homo sapiens. 29-JUL-2004 16-OCT-2003. ABO58422; Query Match Best Loc Matches RESULT 7 ABO58422 H L X B X B X B X B X B X B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X C B X ద ð

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ADM05323;
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                                                                             The invention relates to a nucleic acid probe for measuring human gene expression, comprising any of the 27,400 fully defined nucleotide sequences in the specification, or their complements or fragments, and encoding at least 8 amino acids of any of the 6888 amino acid sequences fully defined in the specification. The probe is a single exon probe that the specification. The probe is a single exon probe that hybridises under high stringency conditions to a nucleic acid molecule expressed in human cells or tissues. Also included are a spatially.

Compressed in human cells or tissues. Also included are a spatially.

Compression (comprising a plurality of single exon nucleic acid gene expression (comprising a plurality of single exon nucleic acid adversesably isolatable or amplifiable from the plurality), a single con microarray for measuring human gene expression, a method of configuous amino acide of any of the above—mentioned amino acide above, an ORF-encoded peptide comprising at least 8

Configuous amino acide of any of the above—mentioned amino acide above, nucleosing specifically to a peptide cited above, and sequences (optionally with conservative amino acid substitutions), an isolated antibody that binds specifically to a peptide cited above. The probe or microarrays to a customer desiring to measure gene expression, a method of providing thuman gene expression data by subscription, and a computer-readable crorage medium which contains a database having a plurality of records cited above. The probes may be used as tools for surveying testorage medium which contains a database having a single exon probe cited above. The probes may be used as tools for surveying testorage to detect the presence of expression of a single exon microarrays. In addition, the probes are used in identifying and characterising and characterising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alternative splicing events, in detecting and characterising gross alterations in the genomic locus that includes their exon, in assessing smaller genomic alterations, in priming the synthesis of nucleic acids, or in expressing the ORF-encoded peptide. The present sequence is a human single exon probe protein of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formet directly from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pigA3Cy3GFP plasmid protein product (Cycle3 GFP under an actin promoter).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 81; DB 8; Length 219;
Pred. No. 5e-06;
; Mismatches 0; Indels
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                                               SEQ ID NO 32056; 80pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADR38362 standard; protein; 310 AA.
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100.0%;
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Best Local Similarity
Matches 15; Conserv
surveying tissues.
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Synthetic.
Unidentified.
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                                                                                                                                                                                                                                                                                                                                                                  Introducing foreign gene into insect cell, involves introducing DNA having foreign gene integrated between inverted repeat sequences of piggyBac transposon and piggyBac transposase that acts on inverted repeat sequence.
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Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      into an insect cell. Specifically, it refers to a foreign gene occurring between inverted repeat sequences of a piggyBac transposon and using a piggyBac transposon and using a piggyBac transposon and using a efficiency. The present invention describes the insect cell as that of Lepidoptera insect origin, preferably it is the silk worm Bombyx mori, and stable integration occurs into the genome of this insect using the transposase enzyme. In particular, this gene transfer method uses the plasmid pigA3Cy3GFP which contains a Cycle3 GFP gene expressed under a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      silk worm actin promoter (A) promoter) between a pair of inverted repeat sequences of the transposon (A) promoter. This polypebtide sequence is the protein product from the pigA3Cy3GFP plasmid DNA that represents the silkworm actin promoter controlling expression of the Cycle3 GFP gene given in an exemplification of the invention. NOTE: This sequence is given as an embedded protein in the sequence listing and is not referred to further within the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention relates to a novel method for introducing a foreign gene
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100.0%; Pred. No. 7.2e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page; 25pp; Japanese.
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                                                               10-FEB-2003; 2003JP-00032306.
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                                                                                                                              10-FEB-2003; 2003JP-00032306
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                                                                                                                                                                                                 (TORA ) TORAY IND INC
                                                                                                                                                                                                                                                                   WPI; 2004-608233/59.
N-PSDB; ADR38361.
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les 15; Conserv
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Yamamoto J,
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26-AUG-2004.
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expression vector. Also described is the DNA sequence given in AAZ88225
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Best Local Similarity
Matches 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
AAB12985
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                                                                                                                                                                                                        The invention relates to a novel human polynucleotide and the encoded polypeptide. A polynucleotide of the invention may have a use in gene therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful as a primer for synthesizing the polynucleotide or as a probe for detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are useful in gene therapy, for developing a diagnostic marker or medicines for regulating their expression and activity, or as a target of gene therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A Misgurnus mizolepis growth hormone expression vector - containing DNA
                                                                                                                                                                                                                                                                                                                                                               are useful as pharmaceutical agents. The present sequence represents a
protein sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                            New polynucleotides and polypeptides are useful in gene therapy, developing a diagnostic marker or medicines for regulating their expression and activity, or as a target of gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 342;
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   Masuho Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 81; DB 7;
Pred. No. 8e-06;
     Nagahari K,
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                                                                                                                                                                         Claim 1; SEQ ID NO 4008; 305pp; English
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     Otsuka M,
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100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      encoding a beta-actin gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRHQGVMVGMGQKDS
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   Yoshikawa T,
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
'-hea 15; Conserva
                                       WPI; 2003-723558/69.
N-PSDB; ADM02880.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misgurnus mizolepis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-140126/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KIM C G.
KIM C G.
NOH J G.
CHO K N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kim CG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAZ88225
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 342 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JP2000004889-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-1998;
23-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-JAN-2000
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(NOHJ/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cho KN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (KIMD/)
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     Seki N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 10
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which contains the beta actin gene and beta actin gene controlling site of Misgurnus mizolepis. Also described are: (1) an expression vector containing a growth hormone gene and the beta actin gene controlling site of Misgurnus mizolepis; and (2) a method for the preparation of a high growth transformed Misgurnus mizolepis including a step of finely injecting the above expression vector to fertilised eggs of Misgurnus mizolepis and hatching them. The vector can be used for the expression of useful genes in a fish. The method can reduce the breeding period of Misgurnus mizolepis. The present sequence represents the Misgurnus mizolepis actin amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Treatment for sickle cell anemia comprises administering a reducing agent to inhibit and reverse sickled cell formation in blood.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention provides a treatment for sickle cell anaemia, which comprises administering a reducing agent. The treatment inhibits the formation of irreversible sickled cells (ISC) and reverses ISC formation in the blood. The present sequence represents the human beta-actin protein. The sequence is used in the invention to demonstrate that a distulphide bridge is formed between cystelines 284 and 373 in ISC beta-actin as a post-translational modification. The reducing agent used in the treatment acts to correct this post-translational modification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Beta actin; post translational modification; sickle cell anaemia; irreversibly sickled cell; ISC; treatment.
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Pred. No. 8.8e-06;
Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 374;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 81; DB 3; I
100.0%; Pred. No. 8.8e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALABAMA MEDICAL SCI FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB12985 standard; protein; 374 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human beta-actin protein sequence.
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Best Local Similarity 100.
Matches 15; Conservative
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The present invention describes a Misgurnus mizolepis growth hormone

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AAP61532;

AAP61532
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AAP6
XXX
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AAP6
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This sequence is encoded by a drug resistant structural gene which may be used in the expression vector of the invention. This gene is used as the selective marker in the vector. The resulting vector may be used to transform a thymidine-kinase deleted cell allowing introduction of a foreign structural gene. The transformed cell may be used to produce large amounts of useful protein
                                                                                                                                                                                Expression vector contg. drug resistant marker gene - useful for transformation of thymidine kinase-deleted human cells for high levels of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New cardiac actin gene comprising histidine to arginine or glycine to glutamic acid substitution, useful in the diagnosis of diseases associated with the mutation, specifically idiopathic dilated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chromosome 15q14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Posttranslationaly modified human cardiac actin mutant E361G.
                                                                                                                                                                                                                                                                                                                                                                                                                             Length 375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Wild-type Glu substituted by Gly"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cardiac actin; ACTC; human; gene therapy; IDC; chr
idiopathic dilated cardiomyopathy; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 81; DB 2; Le
100.0%; Pred. No. 8.8e-06;
                                                                                                                                                                                                                                                Disclosure; Page 5-7; 7pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB15017 standard; protein; 375 AA.
                                    92JP-00045939.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 100.
Hes 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38 PRHQGVMVGMGQKDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Olson TM, Keating MT;
                                                                                                                                                                                                                foreign protein prodn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-375488/32.
N-PSDB; AAA73739.
                                                                                                                                 WPI; 1994-094836/12.
                                                                                                 (TOYM ) TOYOBO KK.
                                                                                                                                                N-PSDB; AAQ44861.
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 375 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
                                    31-JAN-1992;
                                                                   31-JAN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-JUN-1998;
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     15-FEB-1994.
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                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    In the example, a beta-actin expression vector providing the beta-actin promoter region, a polylinker and a polyadenylation signal was constructed where the expression construct was present on a vector having a bacterial origin of replication, as well as a marker for selection in a mammalian host. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drug resistant; structural gene; expression vector; selective; marker; transformation; thymidine-kinase deleted cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Beta-actin gene and regulatory elements - used for expression of polypeptide(s) in mammalian host cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 81; DB 1; Length 375; 100.0%; Pred. No. 8.8e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                             Actin fibre; actin film; recombinant beta-actin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example; Page 23-24; 32pp; English.
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                                                                                              AAP61532 standard; protein; 375
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(first entry)
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Query Match 100.
Best Local Similarity 100.
Matches 15; Conservative
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                                                                                                                                                                                                             Sequence of beta-actin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kedes LH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1986-077015/12.
N-PSDB; AAN60172.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 375 AA;
                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                           05-SEP-1985;
                                                                                                                                                                                                                                                                                                                                                                                                           13-SEP-1984;
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                                                                                                                                                            25-MAR-2003
13-SEP-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-OCT-1994
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RESULT 13

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Gaps

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The present invention relates to human cardiac actin (ACTC). Genotypic analyses show that ACTC is linked to idiopathic dilated cardiomyopathy (IDC). The ACTC gene maps to chromosome 15414. Six PCR primer pairs (AAA49020 to AAA49031) have been developed to allow analysis of the six exons of ACTC. Studies of two families with IDC showed the presence of two mutations, one in exon 5 and one in exon 6. The present sequence is a mutant of posttranslationaly modified ACTC without the initial two residues. The mutation is a Glu to Gly mutation at position 361. The ACTC protein may be used in a variety of methods for drug screening and for rational drug design. The ACTC gene may be used to treat IDC by gene therapy. Analysis of the ACTC gene provides early identification of subjects likely to develop or who already have IDC. Note: The present sequence described in AAY94569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human cardiac actin protein after posttranslational modification.
                                                                                                                                                                                                                                                                                                                                                         Score 81; DB 3; Length 375;
Pred. No. 8.8e-06;
Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cardiac actin; ACTC; human; gene therapy; IDC; 15q14; idiopathic dilated cardiomyopathy.
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                                                                                                 Claim 3; Page; 36pp; English.
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                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                           38 PRHOGVMVGMGOKDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Keating MT;
                                                                                                                                                                                                                                                                                                                                  Sequence 375 AA;
                                                                        cardiomyopathy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY94569;
Fri Apr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
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The present sequence is human cardiac actin (ACTC) protein, without the initial Met-Cyg which is posttranslationally removed. Genotypic analyses show that ACTC is linked to idiopathic dilated cardiomyopathy (IDC). The ACTC gene maps to chromosome 15q14. Six PCR primer pairs (AAA49020 to AAA49931) have been developed to allow analysis of the six exons of ACTC. Studies of two families with IDC showed the presence of two mutations,

New cardiac actin gene comprising histidine to arginine or glycine to glutamic acid substitution, useful in the diagnosis of diseases associated with the mutation, specifically idiopathic dilated

2000-375488/32. N-PSDB; AAA49032 Claim 3; Col 61-62; 36pp; English.

cardiomyopathy

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Gaps

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One in exon 5 and one in exon 6. The mutations are G to A in codon 312 (Arg312His) and A to G in codon 361 (Glu361Gly). The ACTC protein may be used in a variety of methods for drug screening and for rational drug design. The ACTC gene may be used to treat IDC by gene therapy. Analysis of the ACTC gene provides early identification of subjects likely to develop or who already have IDC
                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                  ö
                                                                                                                                                              Length 375;
                                                                                                                                                                                                Indels
                                                                                                                                                              100.0%; Score 81; DB 3; I
100.0%; Pred. No. 8.8e-06;
:ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                        completed: April 8, 2005, 10:50:43
                                                                                                                                                                                                                                      1 PRHOGVMVGMGOKDS 15
                                                                                                                                                                                                                                                                    PRHOGVMVGMGQKDS 52
                                                                                                                                                                                                  Conservative
                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                               Sequence 375 AA;
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INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
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6521, Ap
7, Appli
8, Appli
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2, Appli
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53, Appl
7721, Ap
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28861, A
32609, A
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2, Appli
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                                                                      April 8, 2005, 09:58:57; Search time 17.5333 Seconds (without alignments) 63.863 Million cell updates/sec
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/Regrows.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
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US-09-106-217-16

US-09-106-217-16

US-09-916-5131

US-09-919-016-6100

US-09-919-172-3

US-09-919-172-3

US-09-919-016-721

US-09-949-016-721

US-09-949-016-10757

US-09-949-016-10757

US-09-949-016-10757

US-09-949-016-10757

US-09-949-016-10757

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US-09-252-991A-28861
US-09-252-991A-32609
                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                 513545 seqs, 74649064 residues
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Maximum Match 100%
Listing first 45 summaries
                                                - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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28 41 50.6 543 4 US-09-252-991A-18055 Sequence 18055, A 29 40 49.4 812 4 US-09-252-991A-1846 Sequence 18464, A 30 40 49.4 812 4 US-09-540-256 Sequence 3056, Ap 31 40 49.4 86.2 4 US-09-543-681A-6115 Sequence 6315, Ap 31 48.1 334 4 US-09-543-681A-6115 Sequence 6315, Ap 31 48.1 334 4 US-09-949-016-11006 Sequence 11006, A 31 48.1 45.3 4 US-09-522-991A-2180 Sequence 2180, A 31 48.1 817 4 US-09-252-991A-316 Sequence 31634, A 31 46.9 120 4 US-09-252-991A-316 Sequence 31634, A 31 46.9 245 4 US-09-254-991A-316 Sequence 31634, A 31 46.9 245 4 US-09-252-991A-316 Sequence 17336, A 31 46.9 245 4 US-09-252-991A-1793 Sequence 17933, A 40 38 46.9 516 4 US-09-252-991A-1793 Sequence 17933, A 40 38 46.9 552 1 US-08-765-081-6 Sequence 6, Applit 47 38 46.9 652 1 US-08-765-081-6 Sequence 6, Applit 48 37 45.7 62 4 US-09-252-991A-30672 Sequence 22522, A 45.7 62 4 US-09-252-991A-30672 Sequence 22522, A 45.7 62 4 US-09-252-991A-30672 Sequence 22522, A 45.7 62 4 US-09-543-681A-7224 Sequence 7224, Applit 50.00-543-681A-7224 Sequence 7224, Applit 50.00-543-691A-7224 Sequence 7224, Applit 50.0
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# ALIGNMENTS

Gaps

Matches

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Sequence 16, Application US/09106217

Patent No. 6063576

GENERAL INFORMATION:
APPLICANT: Keating, Mark T.
APPLICANT: Olson, Timothy M.
TITLE OF INVENTION: Cardiomyopathy, a Heritable Form of Heart Failure
INUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
STREET: 555 Thirteenth Street, N.W., Suite 701 East
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/106,217
REFERENCE/DOCKET NUMBER: 24615-20039.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEPAK: (202) 887-0763
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acids
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: SAXe, Stephen A.
REGISTRATION NUMBER: 38,609
REFERENCE/DOCKET NUMBER: 2323:
TELEPHONE: 202-783-6040
                                                                                                                                                                                                                                                                                                                                                   1 PRHOGVMVGMGQKDS 15
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MEDIUM TYPE: Floppy disk
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amino acid
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amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRHOGVMVGMGQKDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Washington STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 15; Conserv
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                                                                                                                                                 Gaps
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APPLICANT: KIM, Dong Soo
APPLICANT: KIM, Chul Geun
APPLICANT: NAM, Yoon Kwon
APPLICANT: NOH, Jae Koo
APPLICANT: CHO, Kyou Nam
TITLE OF INVENTION: EXPRESSION VECTOR OF MUD LOACH GROWTH HORMONE GENE
FILE REFERENCE: P06344USO/BAS
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                                                                                                       Score 81; DB 3; Length 374;
Pred. No. 1.9e-06;
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APPLICANT: Van Ooyen, Albert Johannes Joseph
TITLE OF INVENTION: Transformation of Phaffia rhodozyma
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
CITY: Washington, D.C.
COINYRY: Washington, D.C.
ZIP: 20006-1812
                                                                                                                                               0; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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Pred. No. 1.9e-06;
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23-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: KR 98/20255
PRIOR FILING DATE: 1998-06-01
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 374
                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09306446C Patent No. 6372959
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; Sequence 14, Application US/08494151
; Patent No. 5840528
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NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
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ORGANISM: Misgurnus mizolepus
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Best Local Similarity 100.
Matches 15; Conservative
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Best Local Similarity
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; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
US-08-609-236-6
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US-09-306-446C-2
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Sequence 6100, Application US/09949016

Sequence 6100, Application US/09949016

Barent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WIMBER: 00/241,755

PRIOR PELLING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,756

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

TENNAME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Keating, Mark T.
APPLICANT: Olson, Timothy M.
TITLE OF INVENTION: Actin Mutations in Dilated
TITLE OF INVENTION: Cardiomyopathy, a Heritable Form of Heart Failure
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
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  100.0%; Score 81; DB 1; Length 376; 100.0%; Pred. No. 2e-06; tive 0; Mismatches 0; Indels
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STREET: 555 Thirteenth Street, N.W., Suite 701 East
STREET: Tower
CITY: Washington
CITYE: Washington
COUNTRY: U.S.A.
ZIP: 20004
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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APPLICATION NUMBER: US/09/106,217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-106-217-2; Sequence 2, Application US/09106217; Patent No. 6063576; GENERAL INFORMATION:
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ATTORNEY/AGENT INFORMATION:
NAME: Saxe, Stephen A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 15; Conservative
  Query Match
Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                              39 PRHQGVMVGMGQKDS
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                                                                                                                                                                                                                                             US-09-949-016-6100
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                                                                                    APPLICANT: Furness, Michael
APPLICANT: Furness, Michael
APPLICANT: Buchbinder, Jenny
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
FILE REFERENCE: PA-0041 US
CURRENT APPLICATION NUMBER: US/09/976,594
CURRENT FILING DATE: 2000-10-12
RIOR APPLICATION NUMBER: 60/240,409
PRIOR PILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 1143
SOFTWARE: PERL PROGRAM
SQO ID NO 731
LENGTH: 375
TYPE: PRT
ORGANISM: Homo sapiens
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; Patent No. 5710003
; GENERAL INFORMATION:
; GENERAL INFORMATION:
; TITLE OF INVENTION: DIAGNOSTIC TEST FOR DETERMINING
; TITLE OF INVENTION: MALIGNANCY OF SMOOTH MUSCLE TUMORS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & ADDRESSEE: No. 5710003fis
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 1837317CD1
US-09-976-594-731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/588,113
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 81; DB 4; 100.0%; Pred. No. 1.9e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                      ; Sequence 731, Application US/09976594; Patent No. 6673549; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 436
ATTORNEY/ACENT INFORMATION:
NAME: RAID, REDECCA L.
REGISTRATION NUMBER: 35,152
REFERENCE/DOCKET NUMBER: TJU-
TELEPHONICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEPHONE: 215-568-3439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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Best Local Similarity 100.
Matches 15; Conservative
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SEQUENCE CHARACTERISTICS:
LENGTH: 376 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
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STATE: PA
-09-976-594-731
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ORGANISM: Homo Sapiens
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US-09-949-016-7721
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US-09-949-016-9424
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US-09-917-254-53
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APPLICANT: Mutter, George
APPLICANT: Mutter, George
TITLE OF INVENTION: Prognostic Classification of Breast Cancer;
TITLE OF INVENTION: Prognostic Classification of Breast Cancer;
FILE REPERENCE: B0801/7224/GTV)
CURRENT APPLICATION NUMBER: US/09/917,254
CURRENT FILING DATE: 2001-07-27
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 102
SOFTWARE: Patentin Version 3.0
SEQ ID NO 53
LENGTH: 377
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                                                                                                                                                                                                                                                                                                                 0; Indels
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; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6673545 1709118CD1
US-09-919-172-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Faris, Mary
APPLICANT: Faris, Mary
TITLE OF INVENTION: PROSTATE CANCER MARKERS
FILE REPERENCE: PA-0036 US
CURRENT APPLICATION NUMBER: US/09/919,172
CURRENT APPLICATION NUMBER: 60/222,469
PRIOR APPLICATION NUMBER: 60/222,469
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 102,
SOFTWARE: PERL PROGRAM
SEQ ID NO 33
                                                                                                                                                                                                                                                                                                               Mismatches
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; Sequence 53, Application US/09917254
; Patent No. 6703204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 33, Application US/09919172; Patent No. 6673545
                                                                                                                                                                                                                                                             100.0%; Scc
100.0%; Pro
REGISTRATION NUMBER: 38,609
REPERENCE/DOCKET NUMBER: 2323
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-783-6040
RELEFAK: 202-783-6031
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 377 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                       1 PRHOGVMVGMGQKDS 15
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Best Local Similarity 100.03
Matches 15; Conservative
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Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                            , MOLECULE TYPE: protein US-09-106-217-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
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Sequence 9424, Application US/09949016
; Sequence 9424, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF; TITLE OF INVENTION: WIMBER: US/09/949,016
; CURRENT PILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR PILING DATE: 2000-10-03
; PRIOR PILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: PESESE for Windows Version 4.0
; SBQ ID NO 9424
                                                                                                                                                                                                                                                     Sequence 7721, Application US/09949016

Sequence 7721, Application US/09949016

Patent No. 6812339

GENERAL INPORMATION:

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR PAPLICATION NUMBER: 60/237,768

PRIOR PAPLICATION NUMBER: 60/237,768

PRIOR PELING DATE: 2000-10-20

PRIOR PELING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FREESEQ for Windows Version 4.0

SEQ ID NO 7721

LENGTH: 386
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Score 81; DB 4; Length 377;
Pred. No. 2e-06;
; Mismatches 0; Indels
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Query Match
Best Local Similarity 100.0%;
Matches 15; Conservative 0
                                                                                                              1 PRHOGVMVGMGQKDS 15
                                                                                                                                                   40 PRHQGVMVGMGQKDS 54
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Best Local Similarity 100.7
Marches 15, Conservative
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Best Local Similarity
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0; Indels

Mismatches

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15; Conservative

Matches

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Squence 10757, Application US/09949016
Fatent No. 681239
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REPREBACE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
FRIOR PILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-03
FRIOR FILING DATE: 2000-10-03
FRIOR FILING DATE: 2000-10-03
FRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SQO ID NO 10757
LENGTH: 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04.14

PRIOR PILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: PSESES FOR WINDOWS Version 4.0

LENGTH: 404
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; Sequence 11313, Application US/09949016
; Patent No. 6812339
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1 PRHQGVMVGMGQKDS 15
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Best Local Similarity 100.
Matches 15; Conservative
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Best Local Similarity
Matches 15; Conserva
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; ORGANISM: Human
US-09-949-016-11313
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ORGANISM: Human
                                                                                                                          US-09-949-016-10757
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116.718 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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81
1 PRHQGVMVGMGQKDS 15
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 4308, Ap Sequence 4148, Ap Sequence 56, Appl Sequence 32056, A Sequence 4008, Ap Sequence 68, Appl Sequence 93, Appl Sequence 3601, Ap Sequence 184471, Sequence Description Sequence US-10-264-049-3601 US-10-424-599-184471 US-10-264-049-4308 US-10-264-049-4148 US-10-202-31C-56 US-10-002-631C-56 US-10-002-386-32056 US-10-108-260A-4008 US-10-322-281-68 US-10-205-194-93 US-10-36-194-93 US-10-36-331-94 US-10-36-331-94 US-10-36-331-94 US-10-205-331-94 SUMMARIES Match Length DB Result

Sequence 101, App	Sequence 33, Appl	4	4, A	31	Seguence 63, Appl	1436	Seguence 1786, Ap	H	2436		N					.,	Sequence 42770, A	16268		Sequence 179917,		Sequence 45677, A				Ч		22281	Sequence 223492,	28333	Sequence 66124, A
US-10-341-434-101	US-09-919-172-33	US-1	US-10-333-680-4		US-10-322-281-63	US-09-925-301-1436	US-10-369-493-1786		US-10-369-493-2436	US-10-424-599-	US-1	US-1	us-1	US-1			US-10-767-701-42770				US-10-437-963-202420			US-10-338-777-5		US-10-424-599-1	US-10-424-599-1		_	US-10-424-599	US-10-425-114-66124
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376	377	377	377	393	398	413	375	375	375	9	73	108	135	136	197	208	230	248	347	376	376	376	376	377	377	377	377	377	377	377	377
100.0	100.0	100.0	100.0	100.0	100.0	100.0	98.8	98.8	95.6	88.9	88.9	88.9	88.9	88.9	88.9	88.9	88.9	88.9	88.9	88.9	88.9	88.9	88.9	88.9	88.9	88.9	88.9	88.9	88.9	88.9	88.9
81	81	81	81	81	81	81	80	80	75	72	72	72	72	72	72	72	72	72	72	72	72	72	72	72	72	72	72	72	72	72	72
14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

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    Squence 3601, Application US/10264049
; Sequence 3601, Application US/10264049
; Publication NO. US20040005579A1
; GENERAL INFORMATION:
; TITLE OF INVENTION:
; TITLE OF INVENTION:
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA133P1
; CURRENT FAPLICATION NUMBER: US/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 3601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 81; DB 15;
100.0%; Pred. No. 2.2e-06;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 PRHOGVMVGMGOKDS 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39 PRHOGVMVGMGQKDS 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
US-10-264-049-3601
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Appl Appl

RESULT 2

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CTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids FRATURE:
NAME/KEY: MISC FEATURE
LOCATION: (180)
COTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids US-10-264-049-4308
LOCATION: (145)
OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
                                                                                                                               LOCATION: (151)
OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
                                                                                                                                                                                                                                                                 LOCATION: (159)
OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
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Sequence 4148, Application US/10264049

Publication No. US20040005579A1

GENERAL INFORMATION:

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

TITLE REFERENCE: PA13191

CURRENT APPLICATION NUMBER: US/10/264,049

CURRENT APPLICATION NUMBER: PCT/US01/18569

PRIOR FILING DATE: 2001-06-07

PRIOR FILING DATE: 2001-06-07

PRIOR FILING DATE: 2000-06-07

NUMBER OF SEQ ID NOS: 4360

SOFTWARE: Patentin Ver. 3.1

SEQ ID NO 4148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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APPLICANT: Muenster, Matthew
TITLE OF INVENTION: METHODS TO IDENTIFY SIGNAL SEQUENCES
FILE REFERENCE: A34943 090495.0243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 81; DB 15;
100.0%; Pred. No. 4.5e-06;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 81; DB 15;
Pred. No. 4.4e-06;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-002-631C-56; Sequence 56, Application US/10002631C; Sequence 56, Application No. US20030157486Al; GENERAL INFORMATION:
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nes 15; Conservative
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CRGANISM: Homo sapiens
US-10-264-049-4148
                                                                                                NAME/KEY: MISC FEATURE
                                                                                                                                                                                                                               NAME/KEY: MISC FEATURE LOCATION: (159)
                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: MISC FEATURE
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Matches
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      Sequence 184471, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
Cao Yongwei
TITLE OF INVENTION:
PILE OF INVENTION WUMBER:
USAGE OF THE TABLE OF THE TABLE
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OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    equals any of the twenty naturally occurring L-amino acids
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REPERENCE: PA13391
CURRENT APPLICATION NUMBER: US/10/264,049
CURRENT FILING DATE: 2002-10-04
FRIOR FILING DATE: 2001-06-07
PRIOR PELING DATE: 2001-06-07
PRIOR FILING DATE: 2000-06-07
NUMBER: PAPPLICATION NUMBER: US 60/209,467
NUMBER OF SEQ ID NOS: 4360
SOFTWARE: PATCHING DATE: 2100-06-07
SOFTWARE: PATCHING DATE: 2000-06-07
SOFTWARE: PATCHING DATE: 2000-06-07
SOFTWARE: PATCHING DATE: 2000-06-07
SOFTWARE: PATCHING DATE: 2000-06-07
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US-10-424-599-184471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 81; DB 15; 100.0%; Pred. No. 3.1e-06;
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Sequence 4308, Application US/10264049
Publication No. US20040005579A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.
Best Local Similarity 100.
Matches 15, Conservative
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OTHER INFORMATION: Xaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: MISC FEATURE LOCATION: (135)
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NAME/KEY: MISC_FEATURE
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ORGANISM: Glycine max
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Gaps

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Sequence 93, Application US/10205194
| Publication No. US20030134301A1
| GENERAL INFORMATION:
| APPLICANT: Warner-Lambert Company
| APPLICANT: Lee, Kevin
| APPLICANT: Brooksbank, Robert
| APPLICANT: Brooksbank, Robert
| APPLICANT: Pinnock, Robert
| APPLICANT: WINMER: US/10/205,194
| CURRENT APPLICATION NUMBER: GB 0118354.0
| PRIOR FILING DATE: 2001-07-27
| NUMBER OF SEQ ID NOS: 177
| SEQ ID NO 93
| LENGTH: 375
                                                                                                                                                             Gaps
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                                                                                                      Length 342;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: David W Morris
APPLICANT: Marc S. Malandro
APPLICANT: Marc S. Malandro
TITLE OF INVENTION: NOVEL Compositions and Methods in Cancer
FILE REPERENCE: 529452010100
CURRENT APPLICATION NUMBER: US/10/322,281
CURRENT FILING DATE: 2002-12-17
NUMBER OF SEQ ID NOS: 866
SOFTWARE: FastSEQ for Windows Version 4.0
EBOTH NOS: 88
LENGTH: 371
                                                                                                                                                          Indels
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100.0%; Score 81; DB 16; Length 3
Best Local Similarity 100.0%; Pred. No. 8.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels
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                                                                                                      Query Match 100.0%; Score 81; DB 15; Best Local Similarity 100.0%; Pred. No. 7.7e-06; Matches 15; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 68, Application US/10322281; Publication No. US20040126762A1; GENERAL INFORMATION:
                                                                                                                                                                                                             1 PRHOGVMVGMGOKDS 15
                                                                                                                                                                                                                                                                 40 PRHOGVMVGMGQKDS 54
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                           ; ORGANISM: Homo sapiens
US-10-108-260A-4008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Homo sapiens
US-10-322-281-68
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US-10-322-281-68
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US-10-205-194-93
     TYPE: PRT
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Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Penn, Barvid R.
APPLICANT: Penn, Barvid R.
APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Barvid R.
APPLICANT: Penn, Barvid R.
APPLICANT: Penn, Barvid R.
APPLICANT: Penn, Barvid R.
APPLICANT: Penn, SHARRESION ANALYSIS TWO
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AEOMICA-X-2
CURRENT PILLING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
LENGTH: 219
SEQ ID NO 32056
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; APPLICANT: HELIX RESERVET INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1e1 full length cDNA; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4008
; LENGTH: 342
                                                                                                                                                                                                                                                                                                               Length 219;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: MAP TO AC026717.3
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 16
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 23
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 6.8
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 20
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 9.8
OTHER INFORMATION: SWISSPROT HIT: P29751, EVALUE 3.00e-94
US-10-029-386-32056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                            ; Score 81; DB 14;
; Pred. No. 4.8e-06;
0; Mismatches 0;
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CURRENT APPLICATION NUMBER: US/10/002,631C
                     CURRENT FILING DATE: 2001-10-31
PRIOR APPLICATION NUMBER: 60/300,309
PRIOR FILING DATE: 2001-06-21
NUMBER OF SEQ ID NOS: 324
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 56
LENGTH: 219
                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0%;
Matches 15; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                   1 PRHOGVMVGMGOKDS 15
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Matches 15; Conservative
                                                                                                                                                                                                                              ; ORGANISM: Homo sapiens
US-10-002-631C-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-029-386-32056
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US-10-108-260A-4008
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APPLICANT: Lee, Kevin
APPLICANT: Dixon, Alistair
APPLICANT: Brookbank, Robert
APPLICANT: Brookbank, Robert
TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
FILE REFERENCE: WL-A-018199
FILE REFERENCE: WL-A-018199
CURRENT APPLICATION NUMBER: US/10/205,331
CURRENT ELING DATE: 2002-07-27
PRIOR APPLICATION NUMBER: GB 0118354.0
PRIOR PILING DATE: 2001-07-27
NUMBER OF SEQ ID NOS: 117
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-341-434-101

Sequence 101, Application US/10341434

Publication No. US20030215835A1

GENERAL INFORMATION:

APPLICANT: OriGene Technologies

TITLE OF INVENTION: Differentially Regulated Prostate Cancer Genes

TILE REFERENCE: 9U 204 205 A1 205
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Publication No. US20040063101A1

GENERAL INFORMATION:

APPLICANT: Scanlan, Matthew

APPLICANT: Old, Lloyd

TITLE OF INVENTION: Human Sarcoma-Associated Antigens

TITLE OF INVENTION: Human Sarcoma-Associated Antigens

CURRENT APPLICATION NUMBER: US/10/260,708

CURRENT APPLICATION NUMBER: US/10/260,708

CURRENT FILING DATE: 2002-09-30

NUMBER OF SEQ ID NOS: 96

SOFTWARE: Patentin version 3.1

SEQ ID NO 82

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MANNER OF AUGUST 
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Best Local Similarity 100.0%; Pred. No. 8.5e-06;
Matches 15; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 81; DB 15; 100.0%; Pred. No. 8.5e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38 PRHQGVMVGMGQKDS 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Rattus norvegicus FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 15; Conservative
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TYPE: PRT
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: BARRS: US/10/369,493
CURRENT APPLICATION UNMBER: US 60/360,039
PRIOR PELING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 5927
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100.0%; Score 81; DB 14; Length 375;
Best Local Similarity 100.0%; Pred. No. 8.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0
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                                                                                                                                                                                     WS-10-316-253-88

Sequence 88, Application US/10316253

Publication No. US20030162706A1

Publication No. US20030162706A1

Publicature Information

APPLICANT: The Procter & Gamble Company

APPLICANT: Peters, Kevin

APPLICANT: Wang, Feng

APPLICANT: Wang, Seng

APPLICANT: Original Content

TITLE OF INVENTION: Anglogenesis Modulating Proteins

FILE REFERENCE: 8865M

CURRENT FILING DATE: 2002-12-10

PRIOR APPLICATION NUMBER: US 60/355,295

PRIOR APPLICATION NUMBER: US 60/355,295

PRIOR APPLICATION NUMBER: US 60/355,295

NUMBER OF SEQ ID NOS: 308

SOFTWARE: Patentin Version 3.1

FENCENCE OF SEQ ID NOS: 308

SOFTWARE: Patentin Version 3.1
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Publication No. US20030233675A1
GENERAL INFORMATION:
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; Publication No. US20040058326A1
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; ORGANISM: Caenorhabditis elegans
US-10-369-493-5927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 PRHQGVMVGMGQKDS 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-316-253-88
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     38 PRHOGVMVGMGQKDS
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Best Local Similarity
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US-10-369-493-5927
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US-10-205-331-94
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100.0%; Score 81; DB 9; Length 377;
Best Local Similarity 100.0%; Pred. No. 8.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; PEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020119463A1 1709118CD1
US-09-919-172-33
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 33, Application US/09919172
Sequence 33, Application US/09919172
Sequence 33, Application US/09919172
GENERAL INFORMATION:
APPLICANT: Faris, Mary
APPLICANT: Faris, Mary
TITLE OF INVENTION: PROSTATE CANCER MARKERS
FILE REPERENCE: PA-0036 US
CURRENT FILING DATE: 2001-07-30
PRIOR PILICATION NUMBER: 60/222,469
PRIOR PILING DATE: 2000-07-28
SOFTWARE: PERL PROGTAM
SEQ ID NO 33
LENGTH: 377
TYPE: PRT
CRGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search completed: April 8, 2005, 12:50:59 Job time : 43.6667 secs
; PRIOR FILING DATE: 2002-01-15; NUMBER OF SEQ 1D NOS: 238; SOFTWARE: ParentIn version 3.1; SEQ 1D NO 101; LENGTH: 376; TYPE: PRT ORGANISM: Homo sapiens US-10-341-434-101
                                                                                                                                                                                                                                                                       1 PRHOGVMVGMGQKDS 15
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GenCore version 5.1.6
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OM protein - protein search, using sw model

April 8, 2005, 09:58:56 ; Search time 9.3333 Seconds (without alignments) 154.634 Million cell updates/sec Run on:

81 1 PRHQGVMVGMGQKDS 15 US-09-423-351C-5 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries PIR 79:* Database :

1: pirl:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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No.	Score	Match	Length	DB	ar ar	Description
1	81	100.0	98	2	C43616	actin beta, cytoso
7	81	100.0	137	~	A28258	5C - E
m	81	100.0	158	~	I49465	
4	81	100.0	213	~	A61043	actin CA15 - sea s
S	81	100.0	308	7	A03000	actin 3 - fruit fl
9	81	100.0	328	7	S05430	actin beta - grass
7	81	100.0	349	N	B25819	, fetal
8	81	100.0	362	7	A26559	actin type 5, cyto
σ	81	100.0		٦	ATBOB	
10	81	100.0	374	П	ATBOG	actin gamma - bovi
11	81	100.0	374	7	JC5818	gamma-actin - huma
12	81	100.0	375	ч	ATBOSM	ij
13	81	100.0	375	Н	ATRB	actin, skeletal mu
14	81	100.0	375	7	ATRIC	actin beta - rat
15	81	100.0	375	-	A48324	actin beta, cytosk
16	81	100.0	375	Н	ATCHB	beta -
17	81	100.0	375	-	ATHUB	
18	81	100.0	375	П	ATHUG	actin gamma 1 - hu
19	81	100.0	375	Т	ATMSB	
	81	100.0	375	٦	ATMSG	actin gamma - mous
21	81	100.0	375	Н	ATRBB	actin beta, non-mu
22	81	100.0	375	-	S11222	actin gamma, cytos
23	81	100.0	375	~	T25272	hypothetical prote
24	81	100.0	375	~	S71125	actin beta-2, cyto
25	81	100.0	375	7	S71124	beta-1,
56	81	100.0		~	S71126	actin beta, cytoso
27	81	100.0		7	A55001	
28	81	100.0	375	~	A54728	alpha,
59	81	100.0	375	~	S42103	actin - Puccinia g

actin - Phaffia rh	actin gamma, smoot	actin 8 - fruit fl	actin CyI - sea ur	Actin-1A - nematod	actin 87E - fruit	actin - fruit fly	actin, cytosolic -	actin, muscle - st	actin 15A - sea ur	actin - sea urchin	actin gamma, enter	actin - Hydra atte	actin (clone gen3)	actin (clones la a
S70377	ATCHSM	ATFF8	ATURS	A48449	504538	JC1246	JS0189	JS0190	807288	809578	A40261	JQ0154	JN0832	JN0833
7 7	4 ~	Н	-	~	7	~	~	~	~	7	~	7	7	7
375	376	376	376	376	376	376	376	376	376	376	376	376	376	376
100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
81	818	81	81	81	81	81	81	81	81	81	81	81	81	81
30	35	33	34	35	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

actin beta, cytosolic - chicken (fragment) C;Species: Gallus gallus (chicken) C;Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 09-Jul-2004

CjAccesion: C43616
R) Paterson, B.M.; Eldridge, J.D.
Socience 224, 1435-1438, 1984
A; Title: alpha-Cardiac actin is the major sarcomeric isoform expressed in embryonic avia A; Reference number: A43616; MUID:84223949; PMID:6729461
A; Accession: C43616
A; Accession: C43616
A; Residues: 1-86 < PAT>
A; Rosidues: 1-86 < PAT>
A; Rosidues: 1-86 < PAT>
C; Superfemences: UNIPROT:Q90736; GB:K02173; NID:g211054; PIDN:AAA98513.1; PID:g211055
C; Superfemily: actin
C; Keywords: Cytosol; methylated amino acid
F; 73/Modified site: 3'-methylhistidine (His) #status predicted

Gaps ; 0 Query Match 100.0%; Score 81, DB 2, Length 86; Best Local Similarity 100.0%; Pred. No. 3.3e-07; Matches 15; Conservative 0; Mismatches 0; Indels

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# 1 PRHOGVMVGMGQKDS 15 ð 셤

PRHQGVMVGMGQKDS 52 38

actin 5C - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004
C;Accession: A28258
R;Vigoreaux, J.0.; Tobin, S.L.
R;Vigoreaux, J.0.; Tobin, S.L.
A;Title: Stage-specific selection of alternative transcriptional initiation sites from the A;Reference number: A28258; MUID:88112795; PMID:3123314

A; Accession: A28258

A;Molecule type: mRNA A;Residues: 1.137 <VIG> A;Cross=references: UNIPROT:P10987 A;Note: the authors translated the codon GAG for residue 96 as Gly

A;Gene: FlyBase:ActSC A;Cross-references: FlyBase:FBgn0000042 C;Superfamily: actin C;Keywords: methylated amino acid F;74/Modified site: 3'-methylhistidine (His) #status predicted

Score 81; DB 2; Length 137; Pred. No. 5.3e-07; 100.0%; 100.0%; Query Match Best Local Similarity

Matches

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A,Molecule type: DNA
A,Residues: 1-308 <FYR>
A,Cross-references: UNIPROT.P02572
A,Note: there are 68 unsequenced residues between positions 160 and 161. Partial sequence!
A,Note: there authors translated the codon GTT for residue 263 as 11e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Riliu, Z.; Zhu, Z.; Roberg, K.; Faras, A.J.; Guise, K.S.; Kapuscinski, A.R.; Hackett, P.E. Mucleic Acids Res. 17, 5850, 1989
A; Title: The beta-actin gene of carp (Ctenopharyngodon idella).
A; Reference number: S05430; MUID:89345185; PMID:2762162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Alonso, S.; Minty, A.; Bourlet, Y.; Buckingham, M. J. Mol. Evol. 23, 11-22, 1986
A;Title: Comparison of three actin-coding sequences in the mouse; evolutionary relations. A;Reference number: A25819; MUID:86200234; PMID:3084797
A;Accession: B25819
A;Molecule type: mRNA
                                                                                                                                                                     regions are highly conserved but
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ô
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C;Species: Mus musculus (house mouse)
C;Date: 23-Aug-1987 #sequence_revision 23-Aug-1987 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       actin beta - grass carp
Species: Ctenopharyngodon idella (grass carp)
C.pate: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004
C.Accession: S05430
                                     ;Species: Drosophila melanogaster
;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
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                                                                                             C;Accession: A03000
R;Fyrberg, E.A.; Bond, B.J.; Hershey, N.D.; Mixter, K.S.; Davidson, Call 24, 107-116, 1981
A;Title: The actin genes of Drosophila: protein coding regions are PA;Reference number: A03000; MUID:81210174; PMID:6263481
A;Accession: A03000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 328;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Introns: 41/3; 121/3; 268/1
C; Superfamily: actin
C; Krywords: cytoskeleton; methylated amino acid
C; Krywords: cytoskeleton; methylated amino acid
F;73/Modified site: 3.-methylhistidine (His) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Superfamily: actin
C;Seywords: methylated amino acid
C;Keywords: methylated amino acid
F;74/Modified site: 3'-methylhistidine (His) #status predicted
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fly (Drosophila melanogaster) (fragments)
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Pred. No. 1.3e-06;
; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 15; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 1-328 <LIU>
A;Cross-references: UNIPROT:P83751; EMBL:M25013
                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Gene: FlyBase:Act42A
A,Cross-references: FlyBase:FBgn0000043
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Best Local Similarity 100.0%; P:
Matches 15; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Map position: 42A
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                                                                                                                                                                                                                                                                   alpha-cardiac actin - mouse (fragment)
c;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: 149465; 149466
R;Garner, I.; Minty, A.J.; Alonso, S.; Barton, P.J.R.; Buckingham, M.E.
EMBO J. 5, 2559-2567, 1986
A;Title: A 5' duplication of the alpha-cardiac actin gene in BALB/c mice is associated A;Reference number: 149465; MUD:87053822; PMID:3023046
A;Accession: 149465
A;Accession: 149465
A;Residues: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: U-158 <RES>
A;Cross-references: UNIPROT:Q61273; GB:M26775; NID:g191646; PIDN:AAA37165.1; PID:g553858
A;Accession: 149466
A;Retue: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 8-158 <RE2>
A;Cross-references: GB:M26776; NID:g191649; PIDN:AAA37166.1; PID:g553859
A;Cross-references: GB:M26776; NID:g191649; PIDN:AAA37166.1; PID:g553859
A;Experimental source: adult cardiac muscle, BALB/c mice
C;Genetics:
A;Introns: 50/3
C;Superfamily: actin
C;Keywords: cardiac muscle; heart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 4
A61043
actin CA15 - sea squirt (Styela clava) (fragments)
c;Species: Styela clava
C;Species: Styela clava
C;Species: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: A61043
R;Beach, R.L.; Jeffery, W.R.
Dev. Genet. 11, 2-14, 1990
A;Title: Temporal and spatial expression of a cytoskeletal actin gene in the ascidian St A;Reference number: A61043, MUID:90298580; PMID:2361333
A;Reference number: A61043
A;Reference number: A61043
A;Reference not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-213 <mr/>ARBAPA
A;Cross-references: UNIPROFICATION
C;Comment: This sequence is expressed in cells undergoing rapid cell division.
C;Reywords: cytoskeleton; methylated amino acid; mitosis; structural protein
C;Reywords: 2,-methylhistidine (His) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                  Gaps
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Pred. No. 6.2e-07;
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                  Indels
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100.0%; Score 81; DB 2; L
Best Local Similarity 100.0%; Pred. No. 8.4e-07;
Matches 15; Conservative 0; Mismatches 0;
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                  Mismatches
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Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                   39 PRHOGVMVGMGQKDS
                                                                           1 PRHOGVMVGMGOKDS
                  Conservative
                  15;
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RESULT 5 A03000

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Mismatches
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A; Experimental source: monocyte
                                          12
                                                                                                                 51
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Best Local Similarity 100.'
Matches 15; Conservative
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                                          PRHOGVMVGMGQKDS
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Matches
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ATBOG
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ATBOSM
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C.Specides: Bos primigenius tearures (cattle)
C.Accession: E14185; A39105; A02999; A14185
R.Vandekerckhove, J.; Weber, K.
Bur. J. Biochem. 90, 451-462, 1979
A.Atitle: Actin amino-acid sequences. Comparison of actins from calf thymus, bovine brain A.Accession: E14185
A.Accession: E14185
A.Accession: E14185
A.Accession: M.G.; Degen, S.J.F.; Seyfried, C.E.; Morris, D.R.
A.Accession: A.B. 1253-12162, 1983
A.Fitle: Regulation of protein synthesis in mitogen-activated bovine lymphocytes. Analys A.Feference number: A39105, MUID:84032385; PMID:6195151
A.Accession: A39105
A.Acce
                                 A;Cross-references: UNIPROT:Q61275; GB:X03767; GB:J00381; GB:M10652; NID:g49869; PIDN:CA;Superfamily: actin
C;Superfamily: actin
C;Koywords: cardiac muscle; heart; methylated amino acid; muscle; skeletal muscle
F;47/Modified site: 3'-methylhistidine (His) #status predicted
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Cispecies: Assertation: Assertation of the constant of the cons
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Pred. No. 1.4e-06;
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Best Local Similarity 100.0%;
Matches 15; Conservative 0;
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Best Local Similarity 100..
Residues: 1-349 <ALO>
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C;Species: Bos primiganius taurus (cattle)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: B14185; A0299
R;Vandekerckhove, J.; Weber, K.
Eur. J. Blochem. 90, 451-462, 1978
A;Title: Actin amino-acid sequences. Comparison of actins from calf thymus, bovine brain A;Reference number: A14185; MUID:79045349; PMID:213279
A;Accession: B14185
A;Molecule type: protein
A;Residues: 1-374 <VAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Cross-references: UNIPROT:P02571
A,Note: only peptides that differed in composition from the corresponding peptides of ra C;Comment: Vertebrate nonmuscle cells contain two highly conserved cytoskeletal actins, C;Superfamily: actin
C;Superfamily: actin
C;Keywords: blocked amino end; cell motility; cytoskeleton; methylated amino acid; micro F;1/Modified site: blocked amino end (Glu) (probably acetylated) #status experimental F;72/Modified site: 3'-methylhistidine (His) #status predicted
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C;Date: 20-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 09-Jul-2004
C;Accession: JC5818; PC4501
R;Hauschildt, S.; Schwarz, C.; Heine, H.; Ulmer, A.J.; Flad, H.D.; Rietschel, E.T.; Jens Biochem. Biophys. Res. Commun. 241, 670-674, 1997
A;Title: Actin: A target of lipopolysaccharid-induced phosphorylation in human monocytes A;Reference number: JC5818; MUID:98096379; PMID:9434766
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A;Residues: 1-61;84-112;147-190;196-209;215-253;335-358 <HA2>
A;Experimental source: monocyte
C;Comment: This protein is involved in a signal transduction that eventually leads to mo
C;Superfamily: actin
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C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 06-Sep-1996
C;Accession: A02997; S13480
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RiBertrand, R.; Derancourt, J.; Kassab, R.
FEBS.Lett. 345, 113-119, 1994
A;Title: The covalent maleimidobenzoyl-actin-myosin head complex. Cross-linking of the 5
A;Reference number: S44393; MUID:94259162; PMID:8200441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C,Keywords: acetylated amino end, ATP binding, methylated amino acid, muscle contraction F1.1-375/Product: actin #status experimental <MATS.
F;1.476/Proditied site: acetylated amino end (Asp) #status experimental
F;73/Modified site: 3 -methylhistidine (His) #status experimental
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A,Residues: 1-375 <NUD.
A;Cross-references: GB:J00691; NID:g202653; PIDN:AAA40657.1; PID:g202654
C,Cross-references: GB:J00691; NID:g202653; PIDN:AAA40657.1; PID:g202654
C,Comment: Vertebrate nomuscle cells contain two highly conserved cytoskeletal actins,
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Riiiu, Z.; Zhu, Z.; Roberg, K.; Faras, A.; Guise, K.; Kapuscinski, A.R.; Hackett, P.B.
Riiu, S.; Zhu, Z.; Roberg, K.; Faras, A.; Guise, K.; Kapuscinski, A.R.; Hackett, P.B.
A; Title: Isolation and characterization of beta-actin gene of carp (Cyprinus carpio).
A; Reference number: A48324; MUID:92190540; PMID:2134183
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C;Date: 13-Jun-1983 #sequence_revision 13-Jun-1983 #text_change 22-Jun-1999
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C,Species: Cyprinus carpio (common carp)
C,Date: 03-Feb-1994 #sequence_revision 11-Apr-1997 #text_change 09-Jul-2004
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R;Nudel, U.; Zakut, R.; Shani, M.; Neuman, S.; Levy, Z.; Yaffe, D.
Nucleic, Acids Res. 11, 1759-1771, 1983
A;Title: The nucleotide sequence of the rat cytoplasmic beta-actin gene.
A;Reference number: A38571; MUID:83168920; PMID:6300777
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ilarity 100.0%; Pred. No. 1.5e-06;
Conservative 0; Mismatches 0;
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A; Residues: 48 -64 < BER>
A; Experimental source: skeletal muscle
C; Superfamily: actin
                                          A; Experimental source: skeletal muscle
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Best Local Similarity 100.
Matches 15; Conservative
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A; Residues: 1-375 <LIU>
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A. Residues: 1-375 < VAN
A. Residues: 1-375 < VAN
B. Residues: 1-375 < VAN
B. Residues: 1-375 < Southuring and C. Southuring 
R; Vandekerckhove, J.; Weber, K.
Differentiation 14, 123-133, 1979
A; File: The complete amino acid sequence of actins from bovine aorta, bovine heart, bov
tiation.
A; Reference number: A02997; MUID:80047657; PMID:499690
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Gaps

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C;Comment: Vertebrate nonmuscle cells contain two highly conserved cytoskeletal actins, C;Genetics:
A;Introns.
A;Introns.
C;Genetics:
C;Genetics:
C;Superfamily: actin
C;Keywords: acetylated amino end; cell motility; cytoskeleton; methylated amino acid; m;
P;2.375/Product: actin beta, cytoskeletal #status predicted cMAT>
F;2/Modified site: acetylated amino end (App) (in mature form) #status predicted
F;73/Modified site: 3'-methylhistidine (His) #status predicted
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Search completed: April 8, 2005, 10:53:05 Job time : 9.33333 secs

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                                                                                             April 8, 2005, 09:58:56 ; Search time 57.8667 Seconds
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Gapop 10.0 , Gapext 0.5
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Q8awz3 Q9deu3	Q11209 Q8x190	Q88DX4 Q64g12	Q6y250 Q810r5	Q6zyl2 Q7m3y7	Q64913 O6rxk3	072756	Q64i75
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25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Cytoplasmic actin (Fragment).
Bumbyx mori (Silk moth).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
NCBI_TaxID=7091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=Daizo; TISSUE=Silk gland;
Shiomi K., Kajiura Z., Nakagaki M., Yamashita O.;
Baculovirus-mediated efficient ransfer into the central nervous system of the silkworm, Bombyx mori.";
Nihon Sanshigaku Zasshi 72:149-155(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                          Beta actin (Fragment).
Ovis aries (Sheep).
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Caprinae; Ovis
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                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
TISSUE-Abomasum;
Salamusquanathan T., Hickford J.G.H., Savill M., Sykes A.R.;
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AYS66300; AAS68014.1; -.
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Matches 15, Conservative
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SEQUENCE FROM N.A.
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Bukaryota; Metazoa; Platyhelminthes; Turbellaria; Seriata; Tricladida;
Paludicola; Dugesiidae; Schmidtea.
NCBL_TaxID=50054;
Schmidica polychroa.
Bukaryota; Metazoa; Platyhelminthes; Turbellaria; Seriata; Tricladida;
Paludicola; Dugesiidae; Schmidtea.
NCBI_TaxID=50054;
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MEDIANE-99186847; PubMed=9518500; DOI=10.1093/nar/26.8.2031;
Pagotti A., Gabbiani G., Pascolini R., Neuville P.;
Multiple isoform recovery (MIR)-PCR: a simple method for the isolation of related mRNA isoforms."
Nucleic Acids Res. 26:2031-2033(1998).
In alle controls Archins are highly conserved proteins that are involved in various types of cell motility and are ubiquitously expressed in all eukaryotic cells (By similarity).
In MILARITY: Belongs to the actin family.

EMBL, ARO27162; AAC38982.1; -.
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GO:0003774; F:motor activity; IEA.
GO:0005200; F:structural constituent of cytoskeleton; IEA.
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GO; GO:0005884; C:actin filament; IEA.
GO; GO:0005774; F:morco activity; IEA.
GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
InterPro; IPR004001; Actin.
InterPro; IPR004000; Actin.like.
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InterPro; IPR004000; Actin_like.
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PROSITE; PS00406; ACTINS_1; 1.
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PROSITE; PS00406; ACTINS_1; 1.
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01-AUG-1998 (TrEMBLrel. 07,
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Schmidtea polychroa.
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SEQUENCE
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Bukaryota, Metazoa, Platyhelminthes, Turbellaria, Seriata, Tricladida,
Paludicola, Dugesiidae, Schmidtea.
NCBI_TaxID=50054;
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MEDLINE=98186847; PubMed=9518500; DOI=10.1093/nar/26.8.2031;
Pagotti A., Gabbiani G., Pascolini R., Neuville P.;
"Multiple isoform recovery (MIR) -PCR: a simple method for the isolation of related mRNA isoforms.";
Nucleic Acids Res. 26:2031-2033(1998).
-- FUNCTION: Actins are highly conserved proteins that are involved in various types of cell motility and are ubiquitously expressed in all eukaryotic cells (By similarity).
-- SIMILARITY: Belongs to the actin family.
HSSP; PO2577; INM1.
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GO; GO:0003774; F:mctor activity; IEA.
GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
InterPro; IPR004000; Actin_like.
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Last sequence update)
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Last annotation update)
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Pred. No. 3e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                             78 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                             EMBL; AB186491; BAD35130.1; -.
InterPro; IPR004000; Actin_like.
Pfam; PF00022; Actin; 1.
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0
    STRAIN=Daizo; TISSUE=Silk gland;
                                                                                                                                                                                                                                                                                                                                                                                                                                    O1-AUG-1998 (TrEMBLrel. 07, C1 01-AUG-1998 (TrEMBLrel. 07, La 01-JUN-2003 (TrEMBLrel. 24, Lak Actin 1 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PS00406; ACTINS_1; 1.
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100.0%;
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                                                                                                                                                                                                                                                                               1 PRHQGVMVGMGQKDS 15
                                                                                                                                                                                                                                                                                                                  PRHOGVMVGMGQKDS 53
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Best Local Similarity luv...
For 15; Conservative
                                                                                                                                                                                                                Local Similarity 100.
nes 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00190; ACTIN
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061376;
01-AUG-1998 (TEBMELRE
01-AUG-1998 (TEBMELRE
01-UUN-2003 (TEBMELRE
ACTIN 2 (Fragment).
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SEQUENCE
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SEQUENCE
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                            Shiomi K
                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                             061375
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061376
ID 06137
AC 06137
DT 01-AU
DT 01-AU
DT 01-JU
DE ACTI
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061375
1061375
101-AD
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NCBI_TaxID=9913;
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       SO PER PRINCE CONTROL OF THE PRINCE CONTROL 
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                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   phospholying growth factor receptors in the cornea.";
Am. J. Physiol. Cell Physiol. 283:C1646-C1654(2002).
-!- FUNCTION: Actins are highly conserved proteins that are involved in various types of cell motility and are ubiquitously expressed in all eukaryotic cells (By similarity).
-!- SIMILARITY: Belongs to the actin family.
EMBL; AF404278; AAL01885.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Beta-actin (Fragment).
Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
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GO: 60:000384; C:actin filament; IEA.
GO; GO:0003774; F:mctor activity; IEA.
GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Injury-elicited differential transcriptional regulation of
                                                                                             Length 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wang D.-A., Du H., Jaggar J.H., Brindley D.N., Tigyi G.J., Watsky M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 79;
                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                           78 AA; 8299 MW; B9DFF1108E4ADB0E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79 AA; 8420 MW; 05056E4E2AC092F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
Beta actin (Fragment)
Bos taurus (Bovine)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 81; DB 2; I 100.0%; Pred. No. 3.1e-06;
                                                                                               Score 81; DB 2;
Pred. No. 3e-06;
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                                                                                                                                            0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                          PRT;
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InterPro; IPR004000; Actin_like
                                                                                        100.0%;
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                                                                                                                                                                                                                   39 PRHQGVMVGMGQKDS 53
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                                                                                                                                            15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 100.
Les 15; Conservative
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    Structural protein.
                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9986;
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01-DEC-2001
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SEQUENCE
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O9TTW4:
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                                                                                                                                            Matches
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Q95L83
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                 John S.J., Bilodeau-Goeseels S.;
Submitted (OrT-1999) to the EMBL/GenBank/DDBJ databases.
-!- PUNCTION: Actins are highly conserved proteins that are involved in various types of cell motility and are ubiquitously expressed in all eukaryotic cells (By similarity).
-!- SIMILARITY: Belongs to the actin family.
EMBL; AP191490; AAP65984.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                          HSSP; PO2577; INMI.
GO; GO:0005884; C:actin filament; IEA.
GO; GO:0003774; F:motor activity; IEA.
GO; GO:0005700; F:structural constituent of cytoskeleton; IEA.
InterPro; IPR004001; Actin_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO; GO:0005884; C:actin filament; IEA.
GO; GO:0003774; F:motor activity; IEA.
GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 81; DB 2; Length 86; 100.0%; Pred. No. 3.3e-06; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                     80 AA; 9133 MW; 47354ABB7010668D CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 81; DB 2; I 100.0%; Pred. No. 3.1e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86 AA
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PROSITE; PS00406; ACTINS_1; 1.
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Best Local Similarity 100.
Matches 15; Conservative
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NON TER 1
NON TER 80
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NON TER 86
SEQUENCE 86 AA;
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ses 15; Conserv
SEQUENCE FROM N.A.
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Q7ZZI1

RESULT 9

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-!- FUNCTION: Actins are highly conserved proteins that are involved in various types of cell motility and are ubiquitously expressed in all eukaryotic cells (By similarity).
-!- SIMILARITY: Belongs to the actin family.
HSSP, PAYS16551; AP21565.1; -.
HSSP, PAYS684; ILCU.
FlyBase; FBG0066214; Dnov\ActB2.
                                                                                                                                                                                                GO:0005884; C:actin filament; IEA.
GO:0003774; F:motor activity; IEA.
GO:0005200; F:structural constituent of cytoskeleton; IEA.
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FlyBase; FBgn0066281; Dame\ActE2.
                                                                                                                                                                                                                                                                                  InterPro; IPR004001; Actin.
InterPro; IPR004000; Actin_like.
Pfam; PF00022; Actin; 1.
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PROSITE; PS00406; ACTINS_1; 1.
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PROSITE; PS00406; ACTINS_1; 1.
Structural protein.
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Best Local Similarity 100...
These 15; Conservative
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Matches 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   McGowan C., Davidson E.A., Davidson W.S.;
McGowan C., Davidson E.A., Davidson W.S.;
L. Submitted (MAK-2003) to the EMBL/GenBank/DBJ databases.
C. I-FUNCTION: Actins are highly conserved proteins that are involved in various types of cell motility and are ubiquitously expressed in all eukaryotic cells (By similarity).
C. I-SINILARITY: Belongs to the actin family.
REMBL; AY262761; AAP31127.1; -..
REMBL; AY262761; AAP31127.1; -..
ROG; GO:0005840; C:actin filament; IEA.
GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
DR GO; GO:0004000; Actin.
DR InterPro; IPR004001; Actin.
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STRAIN=15010-1031.0;
MEDLINE=22480340; PubMed=12574518; DOI=10.1073/pnas.0336368100;
MILKOOP P.J., Williams B.L., Selegue J.E., Carroll S.B.;
"Drosophila pigmentation evolution: divergent genotypes underlying convergent phenotypes.";
Proc. Natl. Acad. Sci. U.S.A. 100:1808-1813(2003).
                                                                                                                                                                                                                                                                                                                                                                                           Salvelinus alpinus (Arctic char).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Salvelinus.
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=47314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 81; DB 2; Length 91; 100.0%; Pred. No. 3.5e-06; Live 0; Mismatches 0; Indels
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91 AA; 10063 MW; 7118DB6663CD895C CRC64;
                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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Last annotation update)
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PROSITE; PS00406; ACTINS_1; 1.
                                                                                                                                                                                                                                                                                     01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24, 01-MAR-2004 (TrEMBLrel. 26, Beta-actin (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24, 01-MAR-2004 (TrEMBLrel. 26,
                                                                         PRHOGVMVGMGQKDS 52
                                          PRHOGVMVGMGOKDS 15
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Best Local Similarity 100.
Matches 15; Conservative
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                                                                                                                                                                                                                                     PRELIMINARY;
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Name=ActE2;
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**Q86CV4** 

RESULT 10

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Proc. Natl. Acad. Sci. U.S.A. 100:1808-1813(2003).

-!- FUNCTION: Actins are highly conserved proteins that are involved in various types of cell motility and are ubiquitously expressed in all eukaryotic cells (By similarity).

-!- SIMILARITY: Belongs to the actin family.

BMBL; AX165516; AAP12711.1; -.
                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=15010-0951.0; PubMed=12574518; DOI=10.1073/pnas.0336368100; PubMed=12574518; DOI=10.1073/pnas.0336368100; Wittkopp P.J.; Williams B.L.; Selegue J.E.; Carroll S.B.; "Drosophila pigmentation evolution: divergent genotypes underlying
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GO; GO:0003774; F:motor activity; IEA.
GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
InterPro; IPRO04001; Actin.
InterPro; IPRO04001; Actin.
Pfam; PF00022; Actin, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila americana (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                Length 96;
                                                                                                                             Indels
96 AA; 10610 MW; 1454B7D9DD3F3564 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96 AA; 10610 MW; 1454B7D9DD3F3564 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                         ; Score 81; DB 2; I
; Pred. No. 3.7e-06;
0; Mismatches 0;
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; 0

Gaps

RESULT 12 Q9QZB4

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Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Orthopteroidea, Orthoptera, Ensifera, Gryllidae, Gryllinae,
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GO; GO:0003774; F:motor activity; IEA.
GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
                                                                                cytoskeleton; IEA
                                                                                                                                                                                                                                          ; Score 81; DB 2; Length 100;
; Pred. No. 3.9e-06;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 81; DB 2; Length 104; 100.0%; Pred. No. 4e-06; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                     100 AA; 11601 MW; 0E14674471D0019D CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                    GO; GO:0005884; C:actin filament; IEA.
GO; GO:000374; F:mctor activity; IEA.
GO; GO:0005200; F:structural constituent of
InterPro; IPR004001; Actin.
InterPro; IPR004000; Actin.
Pfem; PR0022; Actin; 1.
PRINTS; PR00190; ACTIN.
                                                                                                                                                                                                                                                                                                                                                                                                 104 AA.
in all eukaryotic cells (By similarity)
-!- SIMILARITY: Balongs to the actin family,
BABO9974; BAC56464.1;
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HSSP, P02568; 1P8Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gryllus bimaculatus (Two-spotted cricket).
                                                                                                                                                  PROSITE; PS00406; ACTINS_1; 1.
PROSITE; PS01132; ACTINS_ACT_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
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InterPro, IPR004000, Actin_like.
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PROSITE; PS00406; ACTINS 1; 1.
                                                                                                                                                                                                                                                100.0%;
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                                                                                                                                                                                                                                                          Best Local Similarity 100.
Matches 15; Conservative
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es 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Actin (Fragment).
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SEQUENCE
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Q86SB7
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01-MAY-2000 (TYEMBLrel. 13, Created)
01-MAY-2000 (TYEMBLrel. 13, Last sequence update)
01-OTH-2003 (TYEMBLrel. 24, Last annotation update)
Cytoplasmic actin (Fragment).
Cytoplasmic actin (Fragment).
Cytoplasmic actin (Guinea pig).
Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
Bovinae, Bos.
                                                                                                                                                                                                                                                                                                                                                                  HSSP; P02577; INMI.
GO; GO:0005884; C:actin filament; IEA.
GO; GO:0003774; F:motor activity; IEA.
GO; GO:0003774; F:motor activity; IEA.
InterPro; IPR004001; Actin_like.
InterPro; IPR004000; Actin_like.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 81; DB 2; Length 99; 100.0%; Pred. No. 3.8e-06; ive 0; Mismatches 0; Indels
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2004 (TrEMBLrel. 26, Last annotation update)
Similar to b-actin (Fragment)
Bos taurus (Bovine).
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                                                                                              99 AA
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                                                                                              PRT;
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PROSITE; PS00406; ACTINS_1; 1.
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                            53
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  1 PRHQGVMVGMGQKDS 15
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Best Local Similarity 100...
-hes 15; Conservative
                  39 PRHQGVMVGMGQKDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00022; Actin; 1.
                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Structural protein.
                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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SEQUENCE
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RESULT 13

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Gaps

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-I FUNCTION: Actins are highly conserved proteins that are involved in various types of cell motility and are ubiquitously expressed in all eukaryotic cells (By similarity).

-I- SINILARITY: Belongs to the actin family.

EMBL: U82542; AAB66299.1; -.

HSSP; P10983; 1D4X.
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                                                                                                                           018548;
01-JAN-1998 (TrENBLrel. 05, Created)
01-JAN-1998 (TrENBLrel. 05, Last sequence update)
01-JUN-2003 (TrENBLrel. 24, Last annotation update)
Cytoplasmic actin LvC4 (Fragment).
Name=LvC4;
Lytechinus variegatus (Sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euchinoidea; Temnopleuroida; Toxopneustidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A GO; GO: 0005804; C:actin filament; IEA.

R GO; GO: 0005704; F:motor activity; IEA.

R GO; GO: 0003774; F:motor activity; IEA.

R GO; GO: 0005200; F:structural constituent of cytoskeleton; IEA.

R InterPro; IPR004001; Actin.

R PROMY: PR00400; Actin.

R PRINTS; PR001900; Actin.

R PROSITE; PS00406; ACTINS 1: 1.

R PROSITE; PS01132; ACTINS 1: 1.
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                                                                                           108 AA
                                                                                           PRT;
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Best Local Similarity 100.
Matches 15; Conservative
                                                                                       PRELIMINARY;
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                                                                                           018548
RESULT 15
018548
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Search completed: April 8, 2005, 12:03:08 Job time : 57.8667 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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- protein search, using sw model OM protein April 8, 2005, 09:58:56; Search time 62.4 Seconds (without alignments) 92.971 Million cell updates/sec Run on:

Title:

US-09-423-351C-6 74 1 TFNTPAMYVAIQAVL 15 Perfect score:

Sequence:

**BLOSUM62** Scoring table: 2105692 seqs, 386760381 residues Searched:

Gapop 10.0 , Gapext 0.5

2105692 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* A Geneseq 16Dec04:* geneseqp1980s:* geneseqp1990s:* geneseqp2000s:*geneseqp2001s:* geneseqp2004s:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

OUTPHACES	ID	AAW92532 Aaw92532 Beta-act	AAM13687 Aam13687 Peptide	ABB32618 Abb32618 Peptide	AAM26087 Aam26087 Peptide	ABB27467 Human pep	ABB18116 Abb18116 Protein	AAM65825 Human bon	AAM53448 Human	ABG47471 Human liv	AAM01437 Peptide	ABG35459 Human	AAU33076 Aau33076 Novel	_				ADE31206 Ade31206 Human	ABU70549 Abu70549 Human	AAG50947 Arabidops	AAG05115 Arabidops	ADI63068 Human apo	AAG50946 Arabidops		
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Aag56873 Arabidops Aag56944 Arabidops Aag56944 Arabidops Aag66484 Arabidops Adi63011 Human apo Aag163011 Human apo Aag163072 Arabidops Aag56872 Arabidops Aag56943 Arabidops Aag56943 Arabidops Aag56943 Arabidops Aag56943 Arabidops Aag12985 Human bet Aap12985 Human bet Aap12985 Arabidops Aab12985 Human act Abb77395 Human act Abb77395 Human act Abm64831 Arabidops Abm64831 Arabidops Abb77395 Human act Abm64831 Arabidops	Adf30525 Rat angio Adi63062 Human apo
AAGSO873 AAGSO944 AAGSO944 AAGG4243 AAGG6483 AAGG6483 AAGG80872 AAGG80872 AAGG993 AABG42442 AAGG993 AABG5983 ABR64271 ABR64271 ABR64271 ABR64271 ABR64271 ABR64271	ADF30525 ADI63062
44444444444444444444444444444444444444	5 7 5
	37
0.0000000000000000000000000000000000000	100.0
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96999999999999999999999999999999999999	4 4 5

# ALIGNMENTS

RESULT 1

Peptide substrate; CCT; eukaryotic type II chaperonin complex; cyclin; binding agent; substrate-binding site; SBS; substrate folding; actin; tubulin; treatment; cancer; anticancer drug; viral infection; screening; Beta-actin reference peptide substrate #6. AAW92532 standard; peptide; 15 AA. (first entry) tubulin; treatment reduced toxicity. WO9853322-A1 26-NOV-1998. 26-APR-1999 Synthetic. AAW92532; AAW92532 

98WO-GB001485. 22-MAY-1998; 97GB-00010762. 23-MAY-1997;

(CANC-) INST CANCER RES ROYAL CANCER HOSPITAL.

Liou AK; Hynes G, Willison K,

WPI; 1999-070162/06.

Identifying specific binding agents for substrate binding site in CCT chaperonin complex - also new peptide binding agents and their mimetics, and peptides containing a specific CCT binding site, used for treating cancer.

Disclosure, Fig 10, 97pp; English.

This invention describes a method which uses the CCT (eukaryotic type II chaperonin) complex or part of it, for identifying a binding agent that can occupy a substrate-binding site (SBS) on the CCT complex. By binding to the CCT complex, the binding agents block an SBS so that biological activity of the CCT complex is affected, particularly its ability to fold substrates such as actin, tubulin and cyclin. The binding agents are useful for trearment of cancer, particularly when used in combination with an anticancer drug, or viral infections. Nucleic acid fragments are used to screen for agents, e.g. binding agents that modulate interaction between the CCT complex and a protein that is to be folded. The binding

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells.
agents may target cells that are actively synthesising tubulin etc. (unlike known microtubule-stabilising agents that affect all cells), so should have reduced toxicity for normal cells. AAW92527-W92541 are peptide substrates used in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                          Peptide #121 encoded by probe for measuring cervical gene expression.
                                                                                                                                                    Gaps
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                                                                                                                     Length 15;
                                                                                                                                                   0; Indels
                                                                                                                   100.0%; Score 74; DB 2; I
100.0%; Pred. No. 3.2e-07;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                       AAM13687 standard; protein; 97 AA
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30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-0033468.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-02359P.
04-OCT-2000; 2000GB-00024263.
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                                                                                                                                                                                    1 TENTPAMYVAIQAVL 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         cervical cancer
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                                                                                     Sequence 15 AA;
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The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human footal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human genome-derived single exon nucleic acid probes useful for analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide #124 encoded by probe for measuring placental gene expression.
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                                                                                                                                                                                           Human; foetal liver; gene expression; single exon nucleic acid probe.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 27; SEQ ID NO 25253; 639pp + Sequence Listing; English.
                                                                                                                                                                  Peptide #124 encoded by human foetal liver single exon probe.
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2000US-0207456P.
2000US-00608408.
2000US-00632366.
2000US-0234687P.
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                                                                                        ABB32618 standard; peptide;
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12
            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 97 AA;
                                                                                                                                                                                                                                                  WO200157277-A2.
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27-SEP-2000;
04-OCT-2000;
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Matches
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Gaps

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Ouery Match
100.0%; Score 74; DB 4;
Best Local Similarity 100.0%; Pred. No. 3e-06;
Matches 15; Conservative 0; Mismatches 0;

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from human breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acid probes for measuring gene expression in a sample derived probes with a collection of detectably labelled nucleic acids derived from mENA of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for determining predisposition and/or prognosing breast disease. Gene expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring ene expression, with far less bias than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence is a peptide concoded by a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed sequence in the wipo int/pub/published_pct_sequences
                                                                                                                                                                                                                          New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein #115 encoded by probe for measuring heart cell gene expression.
                                                                                                                                                                                                                                                                                                                                                            The invention relates to a spatially-addressable set of single exon
                                                                                                                                                                                                                                                                                                                claim 27; SEQ ID NO 10435; 327pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, gene expression, heart, microarray, vascular system; cardiovascular disease, hypertension, cardiac arrhythmia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 74; DB 4; Length 97; 100.0%; Pred. No. 3e-06; tive 0; Mismatches 0; Indels
                                                                                                                                               Chen W, Rank DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB18116 standard; protein; 97 AA.
                                                                                                     (MOLE-) MOLECULAR DYNAMICS INC
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26-MAY-2000; 2000US-0207456P.
30-JUN -2000; 2000US-0060B40B.
33-AUG-2000; 2000US-00632366.
                      21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
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                   2000US-0234687P.
2000US-0236359P.
03-AUG-2000; 2000US-00632366.
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Best Local Similarity 100.
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human placenta.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to single exon nucleic acid probes (SENP: see AA131315-AA157546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders
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                      Probe; microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 27; SEQ ID NO 26356; 654pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chen W, Rank DR;
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2000US-0234687P.
2000US-0236359P.
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26-MAY-2000; 2000US-0207456P.
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                                            genetic disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 97 AA;
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21-SEP-2000;
27-SEP-2000;
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Query Match

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                                                                                                                                                                                           The present invention relates to single exon nucleic acid probes for measuring human peare expression in a sample derived from human heart (see ABA21535-ABA41305). The present sequence is a protein encoded by one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, human heart and vascular system e.g. cardiovascular disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human bone marrow expressed probe encoded protein SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 74; DB 4; Length 97; 100.0%; Pred. No. 3e-06; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                            ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                     Claim 15; SEQ ID NO 19886; 530pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rank DR;
                                                                              Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAM65825 standard; protein; 97 AA
                                                    (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hanzel DK, Chen W,
            27-SEP-2000; 2000US-0236359P. 04-OCT-2000; 2000GB-00024263.
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2000US-00632366.
2000US-0234687P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-SEP-2000; 2000US-0236359P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-JAN-2001; 2001WO-US000668
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                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TFNTPAMYVAIQAVL 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TENTPAMYVAIQAVL 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                         15; Conservative
                                                                              Hanzel DK,
                                                                                                     WPI; 2001-488899/53
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                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                      Sequence 97 AA;
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30-JUN-2000;
03-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                              Penn SG,
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Matches
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                                                                                               probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of
Human genome-derived single exon nucleic acid probes useful for analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human brain expressed single exon probe encoded protein SEQ ID NO: 25553.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                        Gaps
                                                                                 present invention provides a number of single exon nucleic acid
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                                                 Example 4; SEQ ID NO 26131; 658pp + Sequence Listing; English.
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                                                                                                                                                                                                                                      Length 97;
                                                                                                                                                                                                                     Score 74; DB 4; Lengtn 3. Pred. No. 3e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rank DR;
                 gene expression in human bone marrow.
                                                                                                                                                                                                                                                                                                                                                                                                                             AAM53448 standard; protein; 97 AA.
                                                                                                                                                                                                                                                                     0;
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2000US-00608408.

2000US-00632366.

2000US-0234687P.

2000US-0236359P.
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Best Local Similarity 100...
These 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-483446/52
                                                                                                                                                                                                     Sequence 97 AA;
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21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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Probe; human; breast disease; breast cancer; development disorder; inflammatory disease; proliferative breast disease; non-carcinoma tumour. Peptide #119 encoded by probe for measuring human breast gene expression.

AAM01437 standard; protein; 97 AA.

(first entry)

09-OCT-2001

AAM01437;

5 TENTPAMYVAIQAVL 19

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RESULT 10
                                  AAM01437
ID AAM0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a single exon nucleic acid probe (SENP) (1) for measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nucleotide sequences given in the specification (or complements/ fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABG47348-ABG5930 represent human liver single exon encoded peptides of the invention. Note: The sequence information for this patent doses not appear in the printed specification but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human adult liver.
                       Gaps
                                                                                                                                                                                                                      Human, liver, cirrhosis, hyperlipoproteinaemia, hyperlipidaemia, hypercholesterolaemia, coronary heart disease.
                       ;
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Score 74; DB 4; Length 97;
Pred. No. 3e-06;
                       0; Indels
                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 27; SEQ ID NO 26119; 658pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ftp.wipo.int/pub/published pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DR;
                                                                                                                                                                                                 Human liver peptide, SEQ ID No 26119.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rank
                                                                                                                            ABG47471 standard; peptide; 97 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MOLE-) MOLECULAR DYNAMICS INC
100.0%;
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03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
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2000US-0207456P.
                                                                                                                                                                                                                                                                                                                                30-JAN-2001; 2001WO-US000664
                                             1 TFNTPAMYVAIQAVL 15
                                                           (first entry)
            Local Similarity 100.
nes 15; Conservative
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Best Local Similarity 100.
Matches 15, Conservative
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                                                                                                                                                                                                                                                                                  WO200157273-A2.
                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                      04-FEB-2000;
26-MAY-2000;
                                                                                                                                                                          25-FEB-2003
                                                                                                                                                                                                                                                                                                         09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Penn SG,
                                                                                                                                                   ABG47471;
  Query Match
                       Matches
                                                                                                       RESULT 9
                                                                                                                  ABG47471
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Novel single exon nucleic acid probe used to measuring gene expression in a human breast.

Chen W, Rank DR;

Hanzel DK,

Penn SG,

WPI; 2001-476286/51

(MOLE-) MOLECULAR DYNAMICS INC

27-SBP-2000; 2000US-0236359P. 04-OCT-2000; 2000GB-00024263.

2000US-0207456P. 2000US-00608408. 2000US-00632366. 2000US-0234687P.

30-JUN-2000; 03-AUG-2000;

21-SEP-2000;

04-FEB-2000; 26-MAY-2000;

29-JAN-2001; 2001WO-US000661.

WO200157270-A2.

09-AUG-2001

Homo sapiens

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                                            The present invention relates to novel single exon nucleic acid probes (see AA100010-AA110067). The present sequence is a peptide encoded by one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosting, grading, staging, monitoring and prognosting diseases of the human breast, particularly those diseases with polygenic aetiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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0
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100.0%; Pred. No. 3e-06;
Claim 27; SEQ ID NO 10177; 322pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                          ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABG35459 standard; peptide; 97 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S TENTPAMYVAIQAVL 19
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nes 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 97 AA;
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Gaps

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1 TENTPAMYVAIQAVL 15

lung cancer; COPD; ILD;
sase; interstitial lung disease;

asthma;

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Human peptide encoded by genome-derived single exon probe SEQ ID 25124
                                              chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary disease; interstitial lung disease; tuberous sclerosis; gaucher's disease; Niemann-Pick disease; Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; pulmonary hypertension;
                                                                                                                                                                                                              26-MAY-2000; 2000US-0207456P.
30-UN-2000; 2000US-00608408.
03-AUG-2000; 2000US-0034687P.
27-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236599P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                                                            (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                              Chen W,
                                                                                                                                                                                      30-JAN-2001; 2001WO-US000665
                                                                                                                                                                                                        2000US-0180312P
       (first entry)
                                           exon brobe;
                                                                                                                 nyaline membrane disease
                                                                                                                                                                                                                                                                                              Hanzel DK,
                                                                                                                                                                                                                                                                                                                WPI; 2002-114183/15.
                                                                                                                                                   WO200186003-A2
                                           single
                                                                                                                                  Homo sapiens
        19-AUG-2002
                                                                                                                                                                                                        04-FEB-2000;
                                                                                                                                                                    15-NOV-2001
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Rank DR

Spatially-addressable set of single exon nucleic acid probes, used to measure gene expression in human lung samples.

Claim 27; SEQ ID NO 25124; 634pp; English.

The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of 12614 nucleic acid sequences mentioned in the specification, or their complements or the 1287 open reading frames derived from the 12614 probes. Also included are a microarray comprising the novel set of probes which hybridise at high stringency to a nucleic acid expressed in the human lung; measuring gene expression in a sample celerived from human lung; measuring qene expression in a sample collection of detectably labeled nucleic acids derived from human lung manning in a eukaryotic genome, comprising (a) algorithmically predicting at least one exon from genomic sequences of the eukaryote; and (b) detecting specific hybridisation of detectably algorithmically predicting at least one exon from genomic sequences of the eukaryote; and (b) detecting specific hybridisation of detectably algorithmically predicting at least one exon from genomic sequences of the eving a fragment identical to the predicted exon, the probe is included in the above mentioned microarray; assigning exons to a single exon comprising (a) identifying exons from genomic sequence by the method above and (b) measuring the expression of each of the exons in several tissues and/or cell types using hybridisation to a single exon comprising one of the exons should be assigned to a single secon of expression of the exons in the tissues and/or cell types indicates that the exons should be assigned to a single gene; a peptide comprising one of 12011 sequences, mentioned in the specification, or encoded by the probes/open reading frames (ORF). The probes are used for gene expression charited and for the study of lung diseases such as atthma, lung analysis, and for identifying exons in a gene, particularly using human contractives the exons in exert and analysis, and for identifying exons in a gene, are inceded to analysis, and for identifying cancer, chronic obstructive pulmonary disease (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatrosis, tubercous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary

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The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells capressing the proteins are useful for identifying a therapeutic agent of for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The profeins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon and an application; as anti-inflammatory agents; and in treatment of leukaemias. ANU29510-AAU33104 represent the amino acid sequences of novel human contains an application.
                                                                                                                                                                                                                                ö
histiccytosis, lymphangioleiomyomtosis, pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary dyskinesis, pulmonary hypertension and hyaline membrane disease. The present sequence is a peptide/protein encoded by a single exon probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 stem cell proliferation; haemalopoiesis; nerve tissue regeneration; immune suppression; immune stimulation; anti-inflammatory; leukaemia.
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                                                                                                                                                                                          Length 97;
                                                                                                                                                                            Score 74; DB 5; Lengtn 97, Pred. No. 3e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                            AAU33076 standard; protein; 137 AA.
                                                                                                                                                                                              100.0%;
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2001US-00770160
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                                                                                                                                                                                              Query Match 100.
Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                          1 TFNTPAMYVAIQAVL
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                                                                                                                                                            Sequence 97 AA;
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26-JAN-2001;
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PGN) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymuclectides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal crivity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders of polypeptide and polymuclectide sequences have applications in disquantic for generatic disorders or other traits to assess biodiversity represent cond to produce other types of data and products dependent on DNA and and can dequences. Aggono10-Agg30377 represent novel human diagnostic amino acid sequences. Aggono10-Agg30377 represent cond not appear in the printed specification, but was obtained in electronic format directly from MIPO at (II) why wip, int/pub/published_pot_esquences
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                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                        Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated polynucleotide and encoded polypeptides, useful in
                                                 ö
                        Length 137;
                                                0; Indels
                        Score 74; DB 4; I
Pred. No. 4.5e-06;
                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 20; SEQ ID NO 45460; 103pp; English.
                                                                                                                                                                                                                                 Novel human diagnostic protein #15092.
                                                                                                                                                         ABG15101 standard; protein; 150 AA.
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                        100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                           31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tang YT;
                                                                                                                                                                                                                                                                                                                                                                    30-MAR-2001; 2001WO-US008631.
                                                                                            70 TENTPAMYVAIQAVL 84
                                                                                                                                                                                                        (first entry)
                                                Conservative
                                                                       1 TFNTPAMYVAIQAVL
          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-639362/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAS79288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 150 AA;
Sequence 137 AA;
                                                                                                                                                                                                                                                                                                                    WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       biodiversity.
                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                         18-FEB-2002
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                                                                                                                                                                                 ABG15101;
                                                                                                                                   RESULT 13
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PRR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed considers. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a cupylypeptide in fissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders convergence to the proposition of mutations in the polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations of the generic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and and to produce other types of data and products dependent on DNA and amino acid sequences. Abgonolo-Abg30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in celectronic format directly from WIDD at.

Etp. wipo.int/pub/published_pct_sequences
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                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder.
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100.0%; Score 74; DB 4; Length 150; 100.0%; Pred. No. 5e-06; ive 0; Mismatches 0; Indels
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Pred. No. 5.7e-06;
                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel human diagnostic protein #26860.
                                                                                                                                                                                                                                                                                                                                                                                                         ABG26869 standard; protein; 166 AA
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23-AUG-2000; 2000US-00649167
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N-PSDB; AAS91056.
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Best Local Similarity
                                  Best Local Similarity
Matches 15; Conserv
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Gaps
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Indels
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              1 TFNTPAMYVAIQAVL 15
15; Conservative
Matches
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137 TFNTPAMYVAIQAVL 151

ABP42912 standard; protein; 168 AA. ABP42912; RESULT 15

Human ovarian antigen HPDQZ65, SEQ ID NO:4044. (first entry) 22-AUG-2002

Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour; ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndrome; PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disorder; urinary system disorder; drug screening; gene therapy; chromosome mapping; forensic analysis; antibody preparation; cytostatic; immunomodulatory; neuroprotective; antiinflammatory; gynaecological; reproductive.

Homo sapiens.

WO200200677-A1

03-JAN-2002.

07-JUN-2001; 2001WO-US018569.

07-JUN-2000; 2000US-0209467P

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA; Birse CE, WPI; 2002-147878/19 N-PSDB; ABQ55989 Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and neurological diseases.

Claim 11; SEQ ID NO 4044; 2922pp; English

The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP4328) and to cDNAs encoding them (ABP54131-ABQ56305), and also encompasses polypeptides 90% identical and polypucleotides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigens polymucleotides, antibodies against human ovarian antigens, and the use of ovarian antigens polymucleotides and polypeptides in diagnosing, treating, prognosing or preventing various ovary and/or breast-related disorders. Such conditions include ovarian cancer and breast cancer, and metastatic tumours of ovarian or breast origin, reproductive system disorders (e.g., infertility, disorders of pregnancy, anovulation, polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic shock syndrome), inflammatory conditions (e.g., mastitis, ophoritis and variantis), immune disorders (e.g., congenital and acquired immunodeficiencies, autoimmune ophoritis, systemic lupus erythematosus), blood-related disorders (e.g., anaemia), cardiovascular disorders, respiratory disorders (e.g., anaemia), cardiovascular disorders and urinary system disorders. Ovarian antigen polypeptides and polynucleotides may also be used in screening for compounds which modulate ovarian antigen or activity. The polynucleotides may 

identification of individuals and in forensic analysis, and the polypeptides may be used as food additives or to prepare antibodies useful in disease diagnosis, drug targeting and phenotyping. The present sequence represents a human ovarian antigen of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO in the further be used for gene therapy, chromosome mapping, identification of individuals and in forensic analysi at ftp.wipo.int/pub/published_pct_sequences 8888888888888

Sequence 168 AA;

Gaps . 0 Length 168; Indels 100.0%; Score 74; DB 5; I 100.0%; Pred. No. 5.7e-06; tive 0; Mismatches 0; Conservative Query Match Best Local Similarity Matches 15; Conserv

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1 TENTPAMYVAIQAVL 15

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12 TENTPAMÝVAIQAVĽ 26

8, 2005, 10:50:45 Search completed: April Job time : 64.4 secs Sequence

10593, A 44726, A 61, Appl 93, Appl 61, Appl 93, Appl 93, Appl

Sequence

Scoring table:

Searched:

Perfect score:

Sequence:

OM protein

Run on:

Sequence Sequence

Appl Appl Appl Appl

Sequence 20619 Sequence 49, A Sequence 49, A Sequence 49, A Sequence 49, A Sequence 10593 Sequence 10593 Sequence 61, A Sequence 61, A Sequence 61, A Sequence 61, A Sequence 61, A

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ACCOUNTY: Houston

Sequence 6, Application US/08609236

Sequence 6, Application US/08609236

Fatent No. 6087398

FAPILICANT: Steven R. Goodman

TITLE OF INVENTION: No. 6087398el Sickle Cell Anemia Treatment

TITLE OF INVENTION: No. 6087398el Sickle Cell Anemia Treatment

CORRESPONDENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: McGregor & Adler, LLP

STREET: 8011 Candle Lane

CITY: Houston

STREET: Texas

COUNTRY: USA

ZIP: 77071
           US-09-248-796A-20619
US-09-949-016-6655
US-09-949-016-7396
US-09-232-200-49
US-09-232-197-49
US-09-232-197-49
US-09-232-197-49
US-09-232-195-49
US-09-232-200-61
US-09-232-197-61
US-09-232-197-61
US-09-232-197-61
US-09-232-201-61
US-09-232-201-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CUMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Ploppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word for Macintosh
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/609,236
FILING DATE: March 1, 1996
CLASSIFICATION: DATA:
APPLICATION NUMBER: 60/002,288
FILING DATE: August 14, 1995
CLASSIFICATION SI4
PRION APPLICATION NUMBER: 60/002,288
FILING DATE: August 14, 1995
CLASSIFICATION NUMBER: 90.002,288
FILING DATE: August 14, 1995
CLASSIFICATION NUMBER: 13, 423
REPREBRUE/DOCKET NUMBER: 15807
TELEPHONE: 713-777-2221
TELEPHONE: 713-777-6908
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                         ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGI: ---
MOLECULE TYPE:
DESCRIPTION: Protein
                STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: Amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FRAGMENT TYPE:
ORIGINAL SOURCE:
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Sequence 6, Appli
Sequence 731, App
Sequence 9424, Ap
Sequence 11313, A
Sequence 16, Appli
Sequence 2, Appli
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10757, A
5, Appli
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                                                                                                         April 8, 2005, 09:58:57; Search time 17.5333 Seconds (without alignments) 63.863 Million cell updates/sec
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/cgn2_6/ptodata/1/jaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/jaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/jaa/BCOMB.pep:*
/cgn2_6/ptodata/1/jaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/jaa/PCTUS_COMB.pep:*
                GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-949-016-11313
US-09-106-217-16
US-09-949-016-6100
US-09-949-016-6100
US-09-919-172-33
US-09-917-254-53
US-09-949-016-7721
US-09-949-016-10757
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US-09-949-016-8556
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US-09-538-092-1109
US-09-538-092-1110
US-09-949-016-6656
US-09-949-016-8452
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US-09-306-446C-2
US-08-494-151-14
US-08-261-206A-77
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                                                                                                                                                                                                                                                                                        513545 segs, 74649064 residues
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                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                              - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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1 TFNTPAMYVAIQAVL 15
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Maximum DB seq length: 200000000
                                                                                                                                                                           US-09-423-351C-6
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Query
Match Length D
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Result

Gaps

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Sequence 11313, Application US/09949016

Sequence 11313, Application US/09949016

Patent No. 681239

GENERAL INFORMATION:

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOAD1307

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFFWARE: FEASESEQ for Windows Version 4.0
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Sequence 10. 6063576

GENERAL INFORMATION:

APPLICANT: Kearing, Mark T.

APPLICANT: Olson, Timothy M.

TITLE OF INVENTION: Actin Mutations in Dilated

TITLE OF INVENTION: Cardiomyopathy, a Heritable Form of Heart Failure

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                     Indels
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STREET: 555 Thirteenth Street, N.W., Suite 701 East
STREET: Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATEMETH Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/106,217
                Pred. No. 1.4e-05;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 74; DB 4;
; Pred. No. 1.4e-05;
0; Mismatches 0;
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NAME: Saxe, Stephen A.
NEGESTRATION NUMBER: 38,609
REFERENCE/DOCKET NUMBER: 2323-125
100.0%; Pre-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
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                                                                                     1 TFNTPAMYVAIQAVL 15
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Best Local Similarity 100.
Matches 15; Conservative
                  Best Local Similarity 100.
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U
                                                                                                                                                                                                                    JS-09-949-016-11313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 11313
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US-09-976-594-731

Sequence 731, Application US/09976594

Sequence 731, Application US/09976594

Sequence 731, Application US/09976594

GENERAL INCORMATION:

APPLICANT: Furness, Michael

APPLICANT: Buchbinder, Jenny

TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS

FILE REFERENCE: PA-0041 US

CURRENT FILING DATE: 2001-10-12

PRIOR FILING DATE: 2000-10-12

NUMBER OF SEQ ID NOS: 1143

SEQ ID NO 731

LENGTH: 375
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Sequence 9444, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:
TITLE OF INVENTENCY FOLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERRINCE: CL001307

CURRENT APPLICATION NUMBER: 00/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR PILING DATE: 2000-10-20

PRIOR PADLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 9424

LENGTH: 399
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                                                                                                                                   Length 374;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 1837317CD1
US-09-976-594-731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 74; DB 4; 1
100.0%; Pred. No. 1.3e-05;
                                                                                                                                   Score 74; DB 3; I
Pred. No. 1.3e-05;
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                                                                                                                                      Query Match 100.
Best Local Similarity 100.
Matches 15; Conservative
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Matches 15; Conservative
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ORGANISM: Homo sapiens
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US-09-949-016-9424
                           TISSUE TYPE
                                                CELL TYPE:
CELL LINE:
US-08-609-236-6
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Query Match

Gaps

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RESULT 8
US-09-106-217-2
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                                                                                                                                                                                                                  93.2%; Score 69; DB 3; Length 375; 93.3%; Pred. No. 0.00011; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: MCHUGH, Kirk M.
TITLE OF INVENTION: DIAGNOSTIC TEST FOR DETERMINING
TITLE OF INVENTION: MALIGNANCY OF SMOOTH MUSCLE TUMORS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & STRESSEE: No. 5710003ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION NUMBER: US/08/588,113
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08588113
Patent No. 5710003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Ralph, Rebecca L.
REGISTRATION NUMBER: 35,152
REFERENCE/DOCKET NUMBER: TJUTELECOMMUNICATION INFORMATION:
TELECOMMUNICATION: TELEPHONE: 215-568-3100
              TELEPHONE: 202-783-6040
TELEFAX: 202-783-6031
INFORMATION FOR SEQ ID NO: 16: SEQUENCE CHARACTERISTICS: LENGTH: 375 amino acids
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                126 TFNVPAMYVAIQAVL 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 376 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TFNTPAMYVAIQAVL 15
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Best Local Similarity 93.3<sup>3</sup>
Matches 14; Conservative
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                                                                                                                                    TOPOLOGY: linear; MOLECULE TYPE: protein US-09-106-217-16
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Best Local Similarity
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TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 6
US-08-588-113-2
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RESULT 7 US-09-949-016-6100 ; Sequence 6100, Application US/09949016

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SERVERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-1,755
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR FILING DATE: 2000-10-03
PRIOR PELICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR RILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SSOFTWARE: PRACESEQ for Windows Version 4.0
SSO ID NO 6100
LENGTH: 376
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Patent No. 6063576
GENERAL INFORMATION:
APPLICANT: Keating, Mark T.
APPLICANT: Olson, Timothy M.
TITLE OF INVENTION: Actin Mutations in Dilated
TITLE OF INVENTION: Cardiomyopathy, a Heritable Form of Heart Failure
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/106,217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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NAME: Saxe, Stephen A.
REGISTRATION NUMBER: 38,609
REFRENCE/DOCKET NUMBER: 2323-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-783-6040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  127 TFNVPÁMÝVAIQÁVĽ 141
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TFNTPAMYVAIQAVL 15
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Best Local Similarity 93.33
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-949-016-6100
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ZIP: 20004
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; ORGANISM: Human
US-09-949-016-10757
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ORGANISM: Human
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APPLICANT: Mutter, George
APPLICANT: Baak, Jan
ITLLE OF INVENTION: Prognostic Classification of Breast Cancer
FILE REFERENCE: B0801/7224(JRV)
CURRENT APPLICATION NUMBER: US/09/917,254
CURRENT FILING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: US 60/222,093
PRIOR FILING DATE: 2000-07-28
Query Match 93.2%; Score 69; DB 3; Length 377; Best Local Similarity 93.3%; Pred. No. 0.00011; Matches 14; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93.2%; Score 69; DB 4; Length 377; 93.3%; Pred. No. 0.00011; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673545 1709118CD1
US-09-919-172-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 69; DB 4; I Pred. No. 0.00011;
                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Faris, Mary
APPLICANT: Turner, Christopher M.
TITLE OF INVENTION: PROSTATE CANCER MARKERS;
FILE REFERENCE: PA-0036 US
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/222,469
PRIOR APPLICATION NUMBER: 60/222,469
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 102
SOFTWARE: PERL PROGRAM
SEQ ID NO 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                           Sequence 33, Application US/09919172 Patent No. 6673545
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US-09-917-254-53
; Sequence 53, Application US/09917254
; Patent No. 6703204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 102
SOFTWARE: Patentin version 3.0
SEQ ID NO 53
LENGTH: 377
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128 TFNVPAMYVAIQAVL 142
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Best Local Similarity 93.3%;
Matches 14; Conservative
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                                                                                                                        128 TFNVPAMYVAIOAVL 142
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                                                                                   1 TFNTPAMYVAIQAVL 15
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Matches 14; Conservative
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CORGANISM: Homo Sapiens
US-09-917-254-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
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RESULT 11

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Sequence 10777, Application US/09949016

Sequence 10777, Application US/09949016

Batent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

ITILE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOOL1307

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 10757

LENGTH: 402

TYPE: PRI
                                                    APPLICANT: UNIVERMATION:
APPLICANT: UNIVER, J. Craig et al.
APPLICANT: UNIVER, J. Craig et al.
APPLICANT: UNIVER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-10-20
PRIOR PELING DATE: 2000-10-20
PRIOR PELING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOUTHARD: PRESEQ FOR Windows Version 4.0
SEQ ID NO 7721
LENGTH: 386
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93.2%; Score 69; DB 4; I
Best Local Similarity 93.3%; Pred. No. 0.00012;
Matches 14; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 93.2%; Score 69; DB 4; I Best Local Similarity 93.3%; Pred. No. 0.00011; Matches 14; Conservative 0; Mismatches 1;
Sequence 7721, Application US/09949016 Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 5, Application US/09306446C; Patent No. 6372959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           153 TFNVPAMYVAIQAVL 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            137 TENVPAMYVAIQAVL 151
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APPLICANT: KIM, Dong Soo
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               APPLICANT: NAM, YOON KWON
APPLICANT: NAM, YOON KWON
APPLICANT: NOH, Jae KOO
APPLICANT: NOH, Jae KOO
APPLICANT: CHO, Kyou Nam
TITLE OF INVENTION: EXPRESSION VECTOR OF MUD LOACH GROWTH HORMONE GENE
FILE REFERENCE: P06344US0/BAS
CURRENT APPLICATION NUMBER: US/09/306,446C
CURRENT FILING DATE: 1999-05-06
PRIOR APPLICATION NUMBER: W 98/20255
PRIOR PILING DATE: 1998-06-01
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: KIM, Dong Soo
APPLICANT: KIM, Chul Geun
APPLICANT: NAM, Yoon Kwon
APPLICANT: NOH, Jae Koo
APPLICANT: CHO, Kyou Nam
TITLE OF INVENTION: EXPRESSION VECTOR OF MUD LOACH GROWTH HORMONE GENE
                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                              Query Match
91.9%; Score 68; DB 3; Length 146;
Best Local Similarity 93.3%; Pred. No. 5.6e-05;
Matches 14; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 14, Application US/08494151
Patent No. 5840528
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Transformation of Phaffia rhodozyma
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TILE REFERENCE: P06344US0/BAS
CURRENT APPLICATION NUMBER: US/09/306,446C
CURRENT FILING DATE: 1999-05-06
PRIOR PILING DATE: 1999-05-05
NUMBER OF SEQ ID NOS: 33
SEQ ID NO 2
LENGTH: 374
TYPE: PRT
ORGANISM: Misgurnus mizolepus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Misgurnus mizolepus
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Chul Geun
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US-09-306-446C-2
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US-08-494-151-14
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                                                                                                                                                                                                                                                                             LENGTH: 146
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  APPLICANT:
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OM protein - protein search, using sw model

April 8, 2005, 10:53:18; Search time 42.6667 Seconds (without alignments) 116.718 Million cell updates/sec Run on:

US-09-423-351C-6 74 1 TFNTPAMYVAIQAVL 15 Perfect score: Sequence:

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1418010 segs, 331997259 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Published Applications AA:* Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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7	74	100.0	168	15	US-10-264-049-4044	Sequence 4044, Ap
m	74	100.0		16	US-10-437-963-169247	Sequence 169247,
4	74	100.0	197	15	US-10-424-599-280810	Seguence 280810,
ß	74	100.0		15	US-10-264-049-4148	Sequence 4148, Ap
9	74	100.0		15	US-10-424-599-282905	Sequence 282905,
7	74	100.0		14	US-10-002-631C-56	Sequence 56, Appl
80	74	100.0		15	US-10-424-599-143226	Sequence 143226,
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26	69	93.2	248	15	US-10-424-599-162684	Sequence 162684,
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29	69	93.2	288	12	US-10-425-114-57500	57500,
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32	69	93.2	376	15	5	Н
33	69	93.2	377	6	US-09-919-172-33	n
34	69	93.2	377	14	US-10-338-777-52	Sequence 52, Appl
35	69	93.2	377	15	US-10-236-031B-64	Φ
36	69	93.2	377	15	US-10-424-599-162009	Sequence 162009,
37	69	93.2	377	72	US-10-424-599-162685	_
38	69	93.2	377	15	10-424	П
39	69	93.2	377	15	10-424	
40	69	93.2	377	16	10-333	Sequence 4, Appli
41	69	93.2	377	16	10-437	
42	69	93.2	377	16	10-437-963-1	1982
43	69	93.2	377	16	US-10-767-701-47239	
44	69	93.2	378	15	US-10-425-114-52458	5245
45	69	93.2	378	15	US-10-425-114-59265	Sequence 59265, A

## ALIGNMENTS

Sequence 33414, Application US/09864761

Sequence 33414, Application US/09864761

Sequence 33414, Application US/09864761

Sequence 33414, Application US/09864761

GENERAL INFORMATION:
APPLICANT: Henral, Sharron G.
APPLICANT: Henral, David R.
APPLICANT: Henral, David R.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID FORESTOR TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXPRESSION ANALYSIS BY MICROARRAY
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID FORCE STOLE SOLO-02-04

CURRENT APPLICATION NUMBER: US 60/180, 312

PRIOR PILING DATE: 2000-02-04

PRIOR PELING DATE: 2000-03-04

PRIOR PELING DATE: 2000-00-03-04

PRIOR APPLICATION NUMBER: US 60/207, 456

PRIOR APPLICATION NUMBER: US 60/207, 666

PRIOR APPLICATION NUMBER: US 60/207, 666

PRIOR APPLICATION NUMBER: PCT/US01/0066

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR PLING DATE: 2001-01-30

PRIOR PLING DATE: 2001-01-30 PRIOR APPLICATION NUMBER: PCT/US01/00665 PRIOR FILING DATE: 2001-01-30 PRIOR APPLICATION NUMBER: PCT/US01/00668 PRIOR FILING DATE: 2001-01-30

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APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Abou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Bring
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT APPLICATION Solved See Thereof for Plant Improvement
FILE REFERENCE: 38-21(4966
SEQ ID NOS: 204966
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APPLICANT: Availabate Thomas J
APPLICANT: Availabate Minas
APPLICANT: About K
APPLICANT: About Thus
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE REPERENCE: 38-21(53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
ESEQ ID NO 280810
LENGTH: 197
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100.0%; Score 74; DB 15; Length 197;
Best Local Similarity 100.0%; Pred. No. 2.1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels
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US-10-424-599-280810
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US-10-437-963-169247
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Pred. No. 1.9e-05;
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OTHER INFORMATION: unsure at all Xaa locations
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; Sequence 280810, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                        Sequence 169247, Application US/10437963 Publication No. US20040123343A1 GENERAL INFORMATION:
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           61 TFNTPAMYVAIQAVL 75
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Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Oryza sativa FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Glycine max
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N: EXPRESED IN BONE WARROW, SIGNAL = 28

N: EXPRESED IN ADULT LIVER, SIGNAL = 24

N: EXPRESED IN BLACENTA, SIGNAL = 87

N: EXPRESED IN BT474, SIGNAL = 78

N: EXPRESED IN BT4100, SIGNAL = 78

N: EXPRESED IN BTALL LIVER, SIGNAL = 37

N: EXPRESED IN HELA, SIGNAL = 45

N: EXPRESED IN HELA, SIGNAL = 40

N: EXPRESED IN HELA, SIGNAL = 40

N: EXPRESED IN HELA, SIGNAL = 40

N: EXTREMAN HIT: BE21130.1, EVALUE 3.00e-50

N: SMISSERCH HIT: 042161, EVALUE 4.00e-51

N: EXT_HUMAN HIT: BE256272.1, EVALUE 4.00e-50
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; Sequence 4040. US20040005579A1
; General Information:
    APPLICANT: Birse et al.
    TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PA133P1
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR PILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: Patentin Ver. 3.1
; SEQ ID NO 4044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 74; DB 15; Length 168; 100.0%; Pred. No. 1.7e-05; tive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 74; DB 9; Length 97; 100.0%; Pred. No. 9.4e-06;
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PRIOR APPLICATION NUMBER: PCT/USO1/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00662
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2000-05-31
PRIOR PLING DATE: 2000-05-31
PRIOR PLING DATE: 2000-05-31
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR PLING DATE: 2000-06-30
PRIOR PLING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SEQ ID NO 33414
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HEART, SIGNAL =
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Best Local Similarity 100.C
Matches 15; Conservative
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Matches 15; Conservative
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ORGANISM: Homo sapiens
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CORGANISM: Homo sapiens
US-10-264-049-4044
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CTHER INFORMATION: E3

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Query Match

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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: La Rovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Can Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 143226
LENGTH: 237
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APPLICANT: La Rosa Thomas J
APPLICANT: Xovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 219;
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                   GENERAL INFORMATION:
APPLICANT: Graff, Jonathon M.
APPLICANT: Muchaeler. Matthon TITLE OF INVENTION: METHODS TO IDENTIFY SIGNAL SEQUENCES;
TITLE OF INVENTION: METHODS TO IDENTIFY SIGNAL SEQUENCES;
FILE REFERENCE: A34943 090495.0243
CURRENT APPLICATION NUMBER: US/10/002,631C;
CURRENT FILING DATE: 2001-10-31
FRICR APPLICATION NUMBER: 60/300,309
FRICR FILING DATE: 2001-06-21
NUMBER OF SEQ ID NOS: 324
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 56
LENGTH: 219
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US-10-424-599-143226
                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 74; DB 14; 100.0%; Pred. No. 2.3e-05;
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LOCATION: (1)..(237)
OTHER INFORMATION: unsure at all Xaa locations
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Publication No. US20040031072A1
GENERAL INFORMATION:
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  US20030157486A1
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Best Local Similarity 100.
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Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                           , ORGANISM: Homo sapiens
US-10-002-631C-56
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ORGANISM: Glycine max
FEATURE:
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US-10-424-599-177530
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Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La ROSA Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICANTON DAMBER: US/10/424,599
CURRENT PLILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 282905
LENGTH: 208
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100.0%; Score 74; DB 15; Length 204;
Best Local Similarity 100.0%; Pred. No. 2.1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                   and Antibodies
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US-10-424-599-282905
                                                                                                                                                                                APPLICANT: Birse et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and
FILE REFERENCE: PA1391
CURRENT APPLICATION NUMBER: US/10/264,049
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: PCT/US01/18569
PRIOR FILING DATE: 2001-06-07
PRIOR FILING DATE: 2000-06-07
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LOCATION: (1)..(208)
OTHER INFORMATION: unsure at all Xaa locations
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                                                                                         US-10-264-049-4148
Sequence 4148, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
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128 TFNTPAMYVAIQAVL 142
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SOFTWARE: Patentin Ver. 3.1
SEQ ID NO 4148
LENGTH: 204
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Matches 15, Conservative
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ORGANISM: Homo sapiens
US-10-264-049-4148
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US-10-424-599-282905
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US-10-002-631C-56
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FEATURE:

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us-iu-zus-194-93
sequence 39 Application US/10205194
publication No. US20030134301A1
GENERAL INFORMATION:
APPLICANT: Warner-Lambert Company
APPLICANT: Dixon, Alistair
APPLICANT: Dixon, Alistair
APPLICANT: Pinnock, Robert
APPLICANT: Procksbank, Robert
APPLICANT: Pinnock, Robert
APPLICANT: Sofo-07-24
PRIOR FILING DATE: 200-07-24
PRIOR FILING DATE: 201-07-27
SOFTWARE: PatentIN Ver. 2.1
SOFTWARE: PatentIN Ver. 2.1
SOFTWARE: PATENT
TYPE: PRT
REMAINS: Rattus rattus
FRANTING: Rattus rattus
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| Sequence 68, Application US/1032281
| Sequence 68, Application US/1032281
| Sequence 68, Maphication No. US20040126762A1
| GENERAL INFORMATION:
| APPLICANT: David W. Morris
| APPLICANT: Marc S. Malandro
| TITLE OF INVENTION: Novel Compositions and Methods in Cancer FILE REFERENCE: 52945201000
| CURRENT APPLICATION NUMBER: US/10/322,281
| CURRENT FILING DATE: 2002-12-17
| NUMBER OF SEQ ID NOS: 866
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 68
| LENGTH: 371
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100.0%; Score 74; DB 14; Length 375;
Best Local Similarity 100.0%; Pred. No. 4.2e-05;
Matches 15; Conservative 0; Mismatches 0; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
100.0%; Score 74; DB 16; Length 371;
Best Local Similarity 100.0%; Pred. No. 4.2e-05;
Matches 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                   Length 299;
                                                                                                                                                                                                               Indels
; TYPE: PRT
; ORGANISM: Glycine max
; PEATURE:
; PEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_93446C.1.pep
US-10-424-599-278431
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                                                                                                                                                      ; Score 74; DB 15;
; Pred. No. 3.3e-05;
0; Mismatches 0;
                                                                                                                                                           100.0%;
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                                                                                                                                                                                                                                                                   1 TENTPAMYVAIQAVL 15
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                                                                                                                                                      Query Match
Best Local Similarity 100.03
Matches 15; Conservative
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US-10-322-281-68
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Fublication No. US2004003107241

GENERAL INPORMATION:

APPLICANT: La Rola Thomas J

APPLICANT: La Rola Thomas J

APPLICANT: La Rola Thomas J

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 278431

LENGTH: 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: As Jack E
APPLICANT: APLANTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53313) B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 52089
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     TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
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100.0%; Score 74; DB 15; Length 261;
Best Local Similarity 100.0%; Pred. No. 2.8e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 74; DB 15; Length 276; 100.0%; Pred. No. 3e-05;
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                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Clone ID: PAT_MRT3847_131325C.1.pep
US-10-424-599-177530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Clone ID: 701149157_FLI.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                        FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 177530
LENGTH: 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 52089, Application US/10425114; Publication No. US20040034888A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TFNTPAMYVAIQAVL 15
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Matches 15; Conservative
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                                                                                                                                                                                         TYPE: PRT
ORGANISM: Glycine max
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US-10-424-599-278431
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Sequence 94, Application US/10205331

Publication No. US20040058326A1

GENERAL INFORMATION:

APPLICANT: Warner-Lambert Company

APPLICANT: Dixon, Aliatair

APPLICANT: Dixon, Aliatair

APPLICANT: Brookebank, Robert

TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain

FILE REFERENCE: WL-A-018199

CURRENT APPLICATION NUMBER: US/10/205,331

CURRENT FILING DATE: 2002-07-24

PRIOR APPLICATION NUMBER: GB 0118354.0

PRIOR PILING DATE: 2001-07-27

NUMBER OF SEQ ID NOS: 117

SOFTWARE PATENTING DATE: 2.01-07-27

NUMBER OF SEQ ID NOS: 117

SEQ ID NO 94

LENGTH: 375
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                                                                                                                                                    Sequence 88, Application US/10316253
; Publication No. US20030162706A1
; GENERAL INFORMATION:
    APPLICANT: The Procter & Gamble Company
    APPLICANT: Thompson, Larry
    APPLICANT: Thompson, Larry
    APPLICANT: Wang, Feng
    APPLICANT: Wang, Feng
    APPLICANT: Wang, Renneth
    TITLE OF INVENTION: Angiogenesis Modulating Proteins
    TULE REFERENCE: 8865M
    CURRENT FILING DATE: 2002-12-10
    PRIOR APPLICATION NUMBER: US/10/316,253
    CURRENT FILING DATE: 2002-02-08
    PRIOR APPLICATION NUMBER: US 60/355,295
    PRIOR PILING DATE: 2002-02-08
    SOFTWARE: PatentIn version 3.1
    SEQ ID NO 88
    LENGTH: 375
    LENGTH: 375
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                            1 TFNTPAMYVAIQAVL 15
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; ORGANISM: Rattus norvegicus
US-10-316-253-88
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ORGANISM: Rattus norvegicus
                                                                                                                     RESULT 14
US-10-316-253-88
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US-10-205-331-94
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Search completed: April 8, 2005, 12:50:59 Job time : 42.6667 secs

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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                 Copyright
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- protein search, using sw model OM protein

April Run on:

8, 2005, 09:58:56 ; Search time 9.33333 Seconds (without alignments) 154.634 Million cell updates/sec

US-09-423-351C-6 74 1 TFNTPAMYVAIQAVL 15 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

	Description	actin beta - piq (	85c - p	3 - E	actin (clone 302)	actin beta - grass	type 5,	ו	actin gamma - bovi	gamma-actin - huma	actin beta - rat	actin beta, cytosk	actin - Acanthamoe	actin beta - chick	actin - slime mold	actin beta - human	actin gamma 1 - hu	actin beta - mouse	actin gamma - mous	actin beta, non-mu	actin gamma, cytos	actin beta-2, cyto	actin beta-1, cyto	actin beta, cytoso	actin beta - goose	gamma,	actin - slime mold	н	•	actin 3-subl - sli
	ID	S39777	\$20097	A03000	S11452	S05430	A26559	ATBOB	ATBOG	JC5818	ATRIC	A48324	ATAX	ATCHB	ATDO	ATHUB	ATHUG	ATMSB	ATMSG	ATRBB	S11222	S71125	S71124	S71126	A55001	A43552	ATFY	A48449	JS0189	C23412
	DB	2	~	7	7	7	~	-	Н	N	н	Н	Н	Н	~	Н	Н	ч	-	ч	Н	7	~	~	~	ч	<del>, -</del> 1	~	7	7
	Length	195	195	308	327	328	362	374	374	374	375	375	375	375	375	375	375	375	375	375	375	375	375	375	375	376	376	376	376	376
æ	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
	Score	74	74	74	74	74	74	74	74	74	74	74	74	74	74	74	74	74	74	74	74	74	74	74	74	74	74	74	74	74
	Result No.	1	8	е	4	ß	9	7	æ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

actin 15 - slime m	actin 4 - Caenorha	actin 1 and actin	actin 2 - Caenorha	hypothetical prote	actin - California	actin (clone 403)	actin 5 - Atlantic	actin 11 - Atlanti	actin 3 - Atlantic	actin beta, cytosk	actin A4 - silkwor	actin A3, cytosoli	actin 1 - rice	actin - common tob	actin 97 - potato
A25084	S27135	S16710	S16709	T24448	843509	S11453	S49481	S49479	S49480	S01077	JC5750	A25135	ATRZ1	831933	820098
~	~	~	~	7	7	7	7	7	~	~	~	7	н	~	7
376	376	376	376	376	376	376	376	376	376	376	376	376	377	377	377
100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
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0	_	7	٣	4	5	9	7	8	6	0		2	e	4	S

# ALIGNMENTS

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actin beta - pig (fragments)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 0'O'Oct-1994 #sequence_revision 12-Apr-1996 #text_change 09-Jul-2004
C;Accession: 839777
R;Adamski, J.; Husen, B.; Thole, H.H.; Groeschel-Stewart, U.; Jungblut, P.W.
R;Adamski, J.; Husen, B.; Thole, H.H.; Groeschel-Stewart, D.; Jungblut, P.W.
A;Title: Linkage of 17-beta-costradiol dehydrogenase to actin by epsilon-(gamma-glutamyl A;Reference number: 839777; MUID:94107247; PMID:8280079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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A; Molecule type: protein
A; Residues: 1-20;21-52;53-79;80-85;86-95;96-116;117-151;152-159;160-195 < ADA>
A; Cross-references: UNIPROT: Q7M3B0
C; Superfamily: actin
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100.0%; Pred. No. 5.2e-06;
tive 0; Mismatches 0; Indels
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Best Local Similarity
Matches 15; Conserv
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# 1 TENTPAMYVAIQAVL 15

# 60 TFNTPAMYVAIQAVL 74 ઠે g

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actin 85c - potato (fragment)
C;Species: Solanum tuberosum (potato)
C;Species: Solanum tuberosum (potato)
C;Date: 22-Nov-1993 #sequence_revision 17-Oct-1997 #text_change 09-Jul-2004
C;Accession: 820097
R;Drouin, G.; Dover, G.A.
J. Mol. Bvol. 31, 132-150, 1990
A;Title: Independent gene evolution in the potato actin gene family demonstrated by phyl A;Reference number: 820092; MUID:91012599; PMID:2120451
A;Accession: 820097
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-195 <DRO>
A;Cross-references: UNIPROT:P30170; EMBL:X55747; NID:g21541; PIDN:CAA39277.1; PID:g13455

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Gaps

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100.0%; Score 74; DB 2; Length 195; 100.0%; Pred. No. 5.2e-06; ive 0; Mismatches 0; Indel8

1 TENTPAMYVAIQAVL 15

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15; Conservative

Best_Local Similarity Matches 15; Conser

A; Introns: 132/1 C;Superfamily: actin C;Keywords: cytoskeleton; structural protein

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Gaps

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actin beta - bovine (tentative sequence)
Cispecies: Bos primigenius taurus (cattle)
Cispecies: Bos primigenius taurus (cattle)
Cidate: 30-Sep-1991 #sequence revision 30-Sep-1991 #text_change 09-Jul-2004
Cidate: 30-Sep-1991 #sequence revision 30-Sep-1991 #text_change 09-Jul-2004
Cidate: 30-Sep-1991 #sequence revision 30-Sep-1991 #text_change 09-Jul-2004
Rivandekerckhove, J.; Weber, K.
Rivandekerckhove, J.; Weber, K.
Rivandekerckhove, J.; Weber, 1978
A; Title: Actin amino-acid sequences. Comparison of actins from calf thymus, bovine brain A; Reference number: Al4185; WUDD:79045349; PMID:213279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: protein
A; Residues: 1-374 «VAN»
A; Residues: 1-374 «VAN»
A; Cross-references: UNIPROT: B60712
A; Note: only peptides that differed in composition from the corresponding peptides of rai
R; Degen, J.L.; Neubauer, M.G.; Degen, S.J.F.; Seyfried, C.E.; Morris, D.R.
Biol. Chem. 258, 12153-12162, 1983
A; Title: Regulation of protein synthesis in mitogen-activated bovine lymphocytes. Analys
A; Reference number: A39105; MUID: 84032385; PMID: 6195151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: mRNA
A;Residues: 76-227;344-374 <DEG>
A;Cross-references: GB:K00622; GB:K00623
A;Note: actins beta and gamma were not distinguished in this study
C;Comment: Vertebrate nonmuscle cells contain two highly conserved cytoskeletal actins, i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Keywords: blocked amino end; cell motility; cytoskeleton; methylated amino acid; micro. F;1/Modified site: blocked amino end (Asp) (probably acetylated) #status experimental F;72/Modified site: 3'-methylhistidine (His) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 actin type 5, cytosolic – chicken
C;Species: Gallus gallus (chicken)
C;Date: 09-Sep-1987 #sequence_revision 09-Sep-1987 #text_change 05-Dec-1997
                                                                                                                                                                                                                                                                                    Length 328;
                                                                                                                                               C;Superfamily: actin
C;Keywords: cytoskeleton; methylated amino acid
F;73/Modified site: 3'-methylhistidine (His) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Keywords: Cytosol, methylated amino acid
F;74/Modified site: 3'-methylhistidine (His) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Accession: £26559
R;Bergsma, D.J.; Chang, K.S.; Schwartz, R.J.
Mol. Cell. Biol. 5, 1151-1162, 1985
A;Reference number: A26559; MUID:85213487; PMID:4000121
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100.0%; Pred. No. 1e-05;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                        100.0%; Score 74; DB 2; I 100.0%; Pred. No. 9.2e-06;
A,Residues: 1-328 <LIU>
A;Cross-references: UNIPROT:P83751; EMBL:M25013
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                    Conservative 0
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Best Local Similarity 100.0
Matches 15; Conservative
                                                                                                                   A; Introns: 41/3; 121/3; 268/1
                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: DNA
A;Residues: 1-362 <BER>
C;Superfamily: actin
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Cispecies: Artemia ap. (brine shrimp)
Cispecies: Asacre, L.
Rimacias, M.T.; Sastre, L.
Nucleic Acids Res. 18, 5219-5225, 1990
A;Title: Molecular cloning and expression of four actin isoforms during Artemia developm
A;Reference number: S11452
A;Molecule type: mRNA
A;Accession: S11452
A;Molecule type: mRNA
A;Cross-references: UNIPROT:P18602; EMBL:X52604; NID:95666; PIDN:CAA36837.1; PID:9829162
C;Superfamily: actin
C;Keywords: methylated amino acid; structural protein
F;25/Modified site: 3'-methylhistidine (His) #status predicted
                                                                                                            C.Species: Drosophila melanogaster.
C.Species: Drosophila melanogaster.
C.Species: Drosophila melanogaster.
C.Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
C.Spacession: A03000
B.J.; Hershey, N.D.; Mixter, K.S.; Davidson, N.
Cell 24, 107-116, 1981
A;Title: The actin genes of Drosophila: protein coding regions are highly conserved but A;Reference number: A03000; MUID:81210174; PMID:6263481
A;Residues: 1-308 cFYR>
A;Molecule type: DNA
A;Molecule type: DNA
A;Mote: there are 68 unsequenced residues between positions 160 and 161. Partial sequenc 5;Note: the authors translated the codon GTT for residue 263 as 11e
A;Note: the Authors translated the codon GTT for residue 263 as 11e
A;Cross-references: Flybase:FBgn0000043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
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C,Species: Ctenopharyngodon idella (grass carp)
C,Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004
C,Accession: S05430
R;Liu, Z.; Ruy, Z.; Roberg, K.; Paras, A.J.; Guise, K.S.; Kapuscinski, A.R.; Hackett,
Nucleic Acids Res. 17, 5850, 1989
A;Title: The beta-actin gene of carp (Ctenopharyngodon idella).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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C,Superfamily: actin
C;Keywords: methylated amino acid
F;74/Modified site: 3'-methylhistidine (His) #status predicted
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100.0%; Pred. No. 9.2e-06;
tive 0; Mismatches 0; Indels
                                                                                           actin 3 - fruit fly (Drosophila melanogaster) (fragments)
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A;Status: translation not shown
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Matches 15, Conservative
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A;Cross-references: UNIPROT:P83750; GB:M24113; NID:g213041; PIDN:AAA68886.1; PID:g213042
A;Note: the authors translated the codon TTC for residue 21 as Pro, AAG for residue 50 a
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C;Superfamily: actin
Kewwords: acetylated amino end; cell motility; cytoskeleton; methylated amino acid; mi
F;2-375/Froduct: actin beta, cytoskeletal #status predicted <MAT>
F;2/Modified site: acetylated amino end (Asp) (in mature form) #status predicted
F;73/Modified site: 3'-methylhistidine (His) #status predicted
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C.Species: A.Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C.Accession: A22886; A03004
R.Nellen, W.; Gallwitz, D.
M. Mol. Biol. 159, 1-18, 1982
A.Title: Actin genes and actin messenger RNA in Acanthamoeba castellanii. Nucleotide se
A.Reference number: A92886; MUID:83033627; PMID:6290670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Keywords: cell motility; cytoskeleton; methylated amino acid; microfilament; mitosis; P;2-375/Product: actin beta #status predicted <MAT> F;73/Modified site: 3'-methylhistidine (His) #status predicted
                                                                                                                                                                                                                                                                                   A.M. Sections 1-375. SMD.
A.Gross-references: GB:100691; NID:g202653; PIDN:AAA40657.1; PID:g202654
C.Comment: Vertebrate nonmuscle cells contain two highly conserved cytoskeletal actins,
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R;Liu, Z.; Zhu, Z.; Roberg, K.; Faras, A.; Guise, K.; Kapuscinski, A.R.; Hackett, P.B. DNA Seq. 1, 125-136, 1990
A;Title: Isolation and characterization of beta-actin gene of carp (Cyprinus carpio). A;Ference number: A48324; MUID:92190540; PMID:2134183
A;Accession: A48324
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                    C;Date: 13-Jun-1983 #sequence_revision 13-Jun-1983 #text_change 22-Jun-1999 C;Accession: A38571; A0299 R;Nudel, U.; Zakut, R.; Shani, M.; Neuman, S.; Levy, Z.; Yaffe, D. Nucleic Acids Res. 11, 1759-1771, 1983 A;Title: The nucleotide sequence of the rat cytoplasmic beta-actin gene. A;Reference number: A38571; MUID:83168920; PMID:630777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  actin beta, cytoskeletal - common carp
C;Species: Cyprinus carpio (common carp)
C;Date: 03-Peb-1994 #sequence_revision 11-Apr-1997 #text_change 09-Jul-2004
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Pred. No. 1.1e-05;
Mismatches 0; Indels
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C;Species: Rattus norvegicus (Norway rat)
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Best Local Similarity 100.
Matches 15; Conservative
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Matches 15; Conservative
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A; Residues: 1-375 <LIU>
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A; Molecule type: DNA
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C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: B14185; A02999
R;Vandekerckhove, J.; Weber, K.
Eur. J. Biochem. 90, 451-462, 1978
A;Ritte: Actin amino-acid sequences. Comparison of actins from calf thymus, bovine brain A;Reference number: A14185; MUID:79045349; PMID:213279
A;Accession: B14185
A;Molecule type: protein
A;Residues: 1-374 <VMNs
A;Cross-references: UNIPROT:P02571
A;Note: only peptides that differed in composition from the corresponding peptides of ra
C;Comment: Vertebrate nonmuscle cells contain two highly conserved cytoskeletal actins,
C;Superfamily: actin
C;Keywords: blocked amino end; cell motility; cytoskeleton; methylated amino acid; micrc
C;Keywords: blocked amino end (Glu) (probably acetylated) #status experimental
F;71/Modified site: 3'-methylhistidine (His) #status predicted
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C;Species: Home sapiens (man)
C;Species: Home sapiens (man)
C;Species: Home sapiens (man)
C;Species: Home sapiens
C;Species: Workers: 20-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 09-Jul-2004
C;Accession: JCS818; PC4501
R;Hauschildt, S.; Schwarz, C.; Heine, H.; Ulmer, A.J.; Flad, H.D.; Rietschel, E.T.; Jens
Biochem. Biochyny. Res. Commun. 241, 670-674, 1997
A;Title: Actin: A target of lipopolysaccharid-induced phosphorylation in human monocytes
A;Reference number: JCS818; MUID:98096379; PMID:9434766
A;Residues: 1-374 cHAU>
A;Residues: 1-374 cHAU>
A;Cross-references: UNIPROT:P02571
A;Residues: 1-61,84-112;147-190;196-209;215-253;335-358 cHA2>
A;Residues: 1-61,84-112;147-190;196-209;215-253;335-358 cHA2>
A;Experimental source: monocyte
A;Accession: PC4501
A;Molecule type: protein
A;Residues: 1-61,84-112;147-190;196-209;215-253;335-358 cHA2>
A;Experimental source: monocyte
C;Comment: This protein is involved in a signal transduction that eventually leads to mc
C;Superfamily: actin
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100.0%; Score 74; DB 1; Length 374; 100.0%; Pred. No. 1.1e-05;
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Best Local Similarity
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nes 15; Conserv
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Matches 15; Conserv
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actin beta
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Best Loc Matches

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Best Loca Matches

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Hanukoglu, I.; Tanese, N.; Fuchs, E. Mol. Biol. 163, 673-678, 1983
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;Molecule type: mRNA
;Residues: 1-375 <PON>
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A, Residues: 1-375 <NGX>
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                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: S67999
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                                                                                                                                                                                                                   A;Accession: A92871
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C;Species: Dictyostelium discoideum
C;Species: Dictyostelium discoideum
C;Species: Dictyostelium discoideum
C;Species: Janec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C;Accession: A93223; A92871; $$67999; A03004
R;Vandekerckhove, J; Weber, K.
Nature 284, 475-477, 1980
A;Title: Vegetative Dictyostelium cells containing 17 actin genes express a single major A;Reference number: A93223; MUID:80143270; PMID:6892652
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C; Keywords: acetylated amino end; cell motility; cytoskeleton; methylated amino acid; mi
F;2-375/Product: actin beta #status predicted <MAT>
F;2/Modified site: acetylated amino end (Asp) (in mature form) #status predicted
F;73/Modified site: 3'-methylhistidine (His) #status predicted
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C;Comment: Vertebrate nonmuscle cells contain two highly conserved cytoskeletal actins,
C;Genetics:
A;Introns: 41/3; 121/3; 268/1; 328/3
A,Accession: A92886
A;Molecule type: DNA
A,Residues: 1.375 <NBL>
A;Residues: 1.375 <NBL>
A;Cossidues: 1.375 <NBL>
C;Comment: There are at least three actin genes in A. castellanii.
C;Genetics: A;Introns: 105/3
A;Introns: 105/3
C;Reywords: methylated amino acid
C;Reywords: methylated amino acid
E;73/Modified site: 3'-methylhistidine (His) #status predicted
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A; Residues: 1-375 < KOSS.
A; Residues: 1-375 < KOSS.
A; Cross-references: WILPOT: P60706; EMBL: X00182
A; Note: the sequence shown follows the authors' translation at position 336
A; Note: the sequence shown follows the authors' translation at position 336
Mol. Cell. Biol. 4, 2498-2508, 1984
A; Title: Isolation and characterization of six different chicken actin genes.
A; Reference number: ISO153; MUID: 85085956; PMID: 6513927
A; Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          actin beta - chicken

C;Species: Gallus gallus (chicken)

C;Species: Gallus gallus (chicken)

C;Date: 31-Mar-1993 #text_change 09-Jul-2004

C;Accession: A20888; IS0154

R;Kost, T.A.; Theodorahis, N.; Hughes, S.H.

Nucleic Acids Res. 11, 8287-8301, 1983

A;Title: The nucleotide sequence of the chick cytoplasmic beta-actin gene.

A;Reference number: A20888; MUID:84169478; PMID:6324080
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100.0%; Pred. No. 1.1e-05;
tive 0; Mismatches 0; Indels
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tes 15; Conserv
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A; Residues: 1-17 < CHA>
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A; Molecule type: mRNA; DNA
A; Residues: 288-375 <MCK>
R; Jungbluth, A.; Eckerskorn, C.; Gerisch, G.; Lottspeich, F.; Stocker, S.; Schweiger, A.
FEBS Lett. 375, 87-90, 1995
A; Title: Stress-induced tyrosine phosphorylation of actin in Dictyostelium cells and loc
A; Reference number: S67999; MUID:96087090; PMID:7498488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: protein
A;Residues: 51-61 <JUN>
C;Comment: Although Dictyostelium may contain 17 actin genes, only one major actin is ex
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C;Species: Homo sapiens (man)
C;Date: 30-Sep-1991 #scart_change 09-Jul-2004
C;Accession: A25168; A37248; S23707; A37247; I39394; S38782; A02999
C;Accession: A25168; A37248; F; Reddy, P.; Kakunaga, T.
R;Nakajima-Iijima, S.; Hamada, H.; Reddy, P.; Kakunaga, T.
Apric, Natl. Acad. Sci. U.S.A. 82, 6137, 1985
A;Hitle: Molecular structure of the human cytoplasmic beta-actin gene: interspecies homo A;Reference number: A25168; MUID:85298307; PMID:2994062
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A; Residues: 1-375 < NAK.
A; Cross-references: UNIPROT: P60709; GB:M10277; NID:g177967; PIDN: AAA51567.1; PID:g177968
A; Note: the authors translated the codon CAG for residue 137 as Glu
R; NG, S: Y.; Gunning, P.; Eddy, R.; Ponte, P.; Leavitt, J.; Shows, T.; Kedes, L.
A; Title: Biol. S, 2720-2732; 1985
A; Title: Evolution of the functional human beta-actin gene and its multi-pseudogene fami
A; Reference number: A37248; MUID:86284634; PMID:3837182
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                                                                                                                                                                 comp
A,Cross-references: UNIPROT:P02577
R;McKeown, M.; Firtel, R.A.
J. Mol. Biol. 151, 593-606, 1981
A;Title: Evidence for sub-families of actin genes in Dictyostelium as determined by A;Reference number: A92871; MUID:82122583; PMID:6276562
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A;Residues: 252-375 <4AA>
A;Cross-references: EMBL:V00478; NID:g28244; PIDN:CAA23745.1; PID:g825616
R;Gunning, P.; Ponte, P.; Okayama, H.; Engel, J.; Blau, H.; Kedes, L.
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100.0%; Score 74; DB 1; Length 375;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels
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Search completed: April 8, 2005, 10:53:05 Job time : 9.33333 secs

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                                                                                                                                                                                           Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                     Minimum DB Maximum DB M
                                                                   OM protein
                                                                                                                                                                                                             Sequence:
                                                                                                                                                                                                                                                                                                 Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Database
                                                                                                    Run on:
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Q6uba0 chelonia my	Q8qfs7 scyliorhinu	Q9nb01 metridium s	Q7xak3 asparagus o	Q8jh59 chelydra se					Q8i9w4 biomphalari	Q8i9w5 biomphalari	Q8i9w6 helisoma an	Q8i9w7 helisoma tr	Q8i9w8 biomphalari
Q6UBA0	Q8QFS7	Q9NB01	Q7XAK3	Q8JH59	QGRX10	Q819W1	Q819W2	Q819W3	Q819W4	Q8I9W5	9M6180	Q819W7	Q819W8
N	~	~	~	~	~	N	~	N	~	7	~	~	~
162	165	170	171	171	173	174	174	174	174	174	174	174	174
100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
74	74	74	74	74	74	74	74	74	74	74	74	74	74
32	33	34	35	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

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TISSUE=Antler;
MEDLINE=9823260; PubMed=9571767;
MEDLINE=9823260; Lost 1097-010X(19980501)281:1<36::AID-JEZ6>3.0.CO;2-D;
DOI=10.1002/(SICI)1097-010X(19980501)281:1<36::AID-JEZ6>3.0.CO;2-D;
Francis S.M., Suttle J.M.;
"Detection of growth factors and proto-oncogene mRNA in the growing tip of red deer (Cervus elaphus) antler using reverse-transcriptase polymerase chain reaction (RT-PCR).";
J. Exp. Zool. 281:36-42(1998).
--- FUNCTION: Actins are highly conserved proteins that are involved in various types of cell motility and are ubiquitously expressed in various types of cell motility and are ubiquitously expressed
                                                                                            Bukaryota; Merazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae;
Cervinae; Cervus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26D0D8EBCE629A61 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2003 (TrEMBLrel. 01, Last sequence update) Actin, cytoplasmic 1 (Beta-actin) (Fragment).
                   58 AA
                                    Created)
                   PRT;
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InterPro; IPR004000; Actin_like.
                                    (TrEMBLrel. 01, (TrEMBLrel. 01,
                                                                                      deer)
                   PRELIMINARY;
                                                                                     Cervus elaphus (Red
                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                           NCBI_TaxID=9860;
                            Q28242;
01-NOV-1996 (
01-NOV-1996 (
                  028242
RESULT 1
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Q818C2
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                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kelley G.O., Beauchamp K.A., Hedrick R.R.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Actins are highly conserved proteins that are involved
in various types of call motility and are ubiquitously expressed
in all eukaryotic cells (By similarity).
-!- SIMILARITY: Belongs to the actin family.
--- SIMILARITY: ANIS108.1;
--- HSSP; PO2568; 1MA9.
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01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Putative beta-actin (Fragment).
Tubifex tubifex (Sludge worm).
Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
Tubificina; Tubificidae; Tubifex.
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Eukaryota, Metazoa, Myxozoa, Myxosporea, Bivalvulida, Platysporina,
Myxobolidae, Thelohanellus.
NCBI_TaxID=215725;
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GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
InterPro; IPR004000; Actin_like.
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         Length 58;
                                                                      0; Indels
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1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative beta-actin (Fragment).
      100.0%; Score 74; DB 2; I
100.0%; Pred. No. 5.3e-06;
iive 0; Mismatches 0;
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PROSITE; PS01132; ACTINS_ACT_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. 23, Created)
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                                                                                                                                                                  7 TENTPAMYVAIQAVL 21
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Query Match
Best Local Similarity 100.
Matches 15; Conservative
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Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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NON TER
SEQUENCE
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Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.

-!-FUNCTION: Actins are highly conserved proteins that are involved in various types of cell motility and are ubiquitously expressed in various types of cells (By similarity).

-!-SIMILARITY: Belongs to the actin family.

RMBJ; AY157012; AAN8097.1; ---

RM HSSP; POS277; INM1.

GO; GO:0015629; C:actin cytoskeleton; IEA.

GO; GO:0015629; C:actin cytoskeleton; IEA.

RO; GO:0015629; C:actin cytoskeleton; IEA.

RO; GO:0015629; C:actin cytoskeleton; IEA.

RD; AR17N; PRO0120; Actin 1:

RRINTS; PRO0120; ACTIN.

RRINTS; PRO0120; ACTIN.

RRINTS; PRO0120; ACTIN.

RRINTS; PRO0122; ACTINS.

RRINTS; PRO01122; ACTINS.
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Eukaryota; Metazoa; Myxozoa; Myxosporea; Bivalvulida; Platysporina;
Myxobolidae; Myxobolus.
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Myxobolidae; Myxobolus.
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GO; GO:0015629; C:actin cytoskeleton; IEA.
GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
InterPro; IPR004000; Actin_like.
Pfam; PF00022; Actin; 1.
PRINTS; PR00190; ACTIN.
                                                                                                                                                                                                                                                                                                                Length 60;
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01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Last annotation update)
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PROSITE; PS01132; ACTINS_ACT_LIKE; 1.
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01-MAR-2003 (TrEMBLrel. 23, Create
01-MAR-2003 (TrEMBLrel. 23, Last s
01-OCT-2003 (TrEMBLrel. 25, Last s
Putative beta-actin (Fragment).
Myxobolus exiguus.
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NON TER 60 6
SEQUENCE 60 AA; 64
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NON TER 1
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SEQUENCE 60 AA, 64
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Best Local Similarity
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Best Local Similarity
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Matches 15; Conservative
                          PRELIMINARY;
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                                                                            Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Actins are highly conserved proteins that are involved in various types of cell motility and are ubiquitously expressed in all eukaryotic cells (By similarity).
-!- SIMILARITY: Belongs to the actin family.
EMBL; ANISOOII; AAN85096.1; -.
HSSP; PO2577; INMI.
GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
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Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Actins are highly conserved proteins that are involved
in various types of cell motility and are ubiquitously expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative beta-actin (Fragment).
Myxobolus muelleri.
Bukaryota; Metazoa; Myxozoa; Myxosporea; Bivalvulida; Platysporina;
Myxobolidae; Myxobolus.
NYSD TAXID=204749;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ô
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GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
InterPro; IPR004000; Actin_like.
Pfam; PF00022; Actin_l.
PRINTS; PR00190; ACTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 74; DB 2; Length 60; Pred. No. 5.5e-06; O; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 AA; 6532 MW; C383DFABD3D424AA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 AA; 6498 MW; 3983D5A1D3D424A7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 74; DB 2; I 100.0%; Pred. No. 5.5e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                in all eukaryotic cells (By similarity).
-!- SIMILARLIY: Belongs to the actin family.
BEL; AY157010; ANN85095.1;
HSSP; P02577; 1NM1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS01132; ACTINS_ACT_LIKE; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TENTPAMYVAIOAVL 15
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Best Local Similarity 100..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00022; Actin; 1
PRINTS; PR00190; ACTIN.
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NCBI_TaxID=204750;
                                                            SEQUENCE FROM N.A
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SEQUENCE
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PSEQUENCE FROM N.A.

Kelley G.O., Beauchamp K.A., Hedrick R.R.;

Lisumital (SEP-2002) to the EMBL/GenBank/DBJ databases.

In all eukaryotic cells (By similarity).

In all eukaryotic cells (By similarity).

EMBL; AVI57008; AAN85093.1; -..

RENEL; AVI57008; AAN85093.1; -..

RO; GO:0015629; C:actin cytoskeleton; IEA.

GO; GO:0015629; R:structural constituent of cytoskeleton; IEA.

RO; GO:00221; Actin; 1.

REMINTS; PRO0192; Actin, 1.

REMINTS; PRO1192; ACTINS.

ROSITE; PROSITE; PROSI SEQUENCE FROM N.A.

Kelley G.O., Beauchamp K.A., Hedrick R.R.;

Li Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.

Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.

Li Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.

Li Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.

Li VINCTION: Actins are highly conserved proteins that are involved in all eukaryotic cells (By similarity).

C.I. FINILARITY: Belongs to the actin family.

REMBL; AX157009; AAN85094.1; -..

REMBL; AX157009; AAN85094.1; -..

RO; GO:0015629; C:actin cytoskeleton; IEA.

RO; GO:0015629; C:actin cytoskeleton; IEA.

RO; GO:0015629; C:actin cytoskeleton; IEA.

RO; GO:0015629; Actin, I.R.

RPINTS; PR00190; ACTIN.

RPINTS; PR00190; ACTIN.

RR. PLINTS; PR01190; ACTIN.

RR. PLINTS; PR01190; ACTIN. Gaps Eukaryota; Metazoa; Myxozoa; Myxosporea; Bivalvulida; Platysporina; Myxobolidae; Myxobolus. NCBI_TaxID=182349; Eukaryota; Metazoa; Myxozoa; Myxosporea; Bivalvulida; Platysporina; Myxobolidae; Myxobolus. NCBI_TaxID=59784; .. 100.0%; Score 74; DB 2; Length 60; 100.0%; Pred. No. 5.5e-06; tive 0; Mismatches 0; Indels 60 AA; 6468 MW; 1483D5A1D3D424B0 CRC64; 60 AA; 6498 MW; 3983D5A1D3D424A7 CRC64; 01-WAR-2003 (TrEMBLrel. 23, Created) 01-WAR-2003 (TrEMBLrel. 23, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Putative beta-actin (Fragment) Myxobolus insidiosus. 01-MAR-2003 (TrEMBLrel. 23, Created)
1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative beta-actin (Fragment). 60 AA. Structural protein.
NON TER 1
NON_TER 60 6
SEQUENCE 60 AA; 64 

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Conservative
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NON TER 1
NON_TER 95 9
SEQUENCE 95 AA; 10
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nes 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        O9JLX9;
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ID Q2
AC Q2
DT 01
DT 01
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Spodoptera frugiperda (Fall armyworm).
Spodoptera frugiperda (Fall armyworm).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
Noctuidae; Amphipyrinae; Spodoptera.
                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidei;
Sparidae; Sparus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -I-FUNCTION: Actins are highly conserved proteins that are involved in various types of cell motility and are ubiquitously expressed in all eukaryotic cells (By similarity).
-I-SIMILARITY: Belongs to the actin family.

EMBL; AY362763; AAQ56183.1; -.

GO; GO:0015629; Cactin cytoskeleton; IEA.

InterPro; IPR004000; Actin_like.
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Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Actins are highly conserved proteins that are involved in various types of cell motility and are ubiquitously expressed in all eukaryotic cells (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Krey G.D., Boukouvala E., Hondrogiannis C.I., Theodoridou M.D., Kalevra V.; Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
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   Length 60;
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                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                          05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Beta-actin (Fragment).
Sparus aurata (Gilthead sea bream).
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01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
100.0%; Score 74; DB 2; L
100.0%; Pred. No. 5.5e-06;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                         68 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                         PRT;
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                                                                                                                                1 TENTPAMYVAIQAVL 15
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Query Match
Best Local Similarity 100.
Matches 15; Conservative
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Best Local Similarity
Local 15; Conserve
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=Sprague-Dawley;
Topozaian M., Auer G., Zacour M., Cernacek P., Ward M.E.;
Submitted (JAN.1999) to the BWBL/GenBank/DDBJ databases.
-!- FUNCTION: Actins are highly conserved proteins that are involved in various types of cell motility and are ubiquitously expressed in all eukaryotic cells (By similarity).
-!- SIMILARITY: Belongs to the actin family.
-!- SIMILARITY: Belongs to the Actin family.
-!- SIMILARITY: BAF31761.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                             cytoskeleton; IEA.
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GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
InterPro; IPR004000; Actin_like.
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                                                                                                                                                                                                                                                                                                                                                                           Length 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                          95 AA; 10656 MW; E0C697FD09770932 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97 AA; 11014 MW; D5CE6E996444EF9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
Beta actin (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                           Score 74; DB 2; 1
Pred. No. 8.8e-06;
-!- SIMILARITY: Belongs to the actin family. EMBL; AF548015; AAN38748.1; -. HSSP; POS577; 1NM1. GO; GO:0015629; C:actin cytoskeleton; IEA. GO; GO:0005200; F:structural constituent of cyt InterPro; IRR004000; Actin_11ke. Piam; PF00022; Actin, 1. PRINYS; PR00190; ACTIN. PROSITE; PS01132; ACTINS_ACT_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97 AA.
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PROSITE; PS01132; ACTINS_ACT_LIKE; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
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(TrEMBLrel. 23, I
(TrEMBLrel. 25, I
                                                                                                                                                                                                                                                                                                                                                                                                       100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 TFNTPAMYVAIQAVL 15
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                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.
Best Local Similarity 100.
Matches 15, Conservative
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TISSUE=Liver;
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NON TER
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Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Actins are highly conserved proteins that are involved in various types of cell motility and are ubiquitously expressed in all eukaryotic cells (By similarity).
-!- SIMILARITY: Belongs to the actin family.
HSSP; P02577; 1NM1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                             MEDLINE-96071113; PubMed=7577717; DOI=10.1016/0960-0760(95)00157-U; Yamada-Mouri N., Hirata S., Hayashi M., Kato J.; "Analysis of the expression and the first exon of aromatase mRNA in
                            Macaca fuscata (Japanese macaque).
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
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GO; GO:0003774; F:motor activity; IEA.
GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO; GO:0015629; C:actin cytoskeleton; IEA.
GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
InterPro: IPR004000; Actin_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Elysia chlorotica (Sea slug).
Bukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Apogastropoda; Heterobranchia; Euthyneura; Opisthobranchia; Sacoglossa; Elysioidea; Elysiidae; Elysia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 74; DB 2; Length 117; 100.0%; Pred. No. 1.1e-05; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 109;
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109 AA; 12333 MW; 64A64E108CDDA54C CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 74; DB 2; 100.0%; Pred. No. 1e-05;
                                                                                                                                                                                                                                                                                                                                                                                                   J. Steroid Biochem. Mol. Biol. 55:17-23(1995).
EMBL; S79782; AAB35618.2; -.
HSSP; P10983; 1D4X.
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Best Local Similarity 100.0%; Pred. No. 1.15
Best Local Similarity 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117 AA
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PROSITE; PS01132; ACTINS_ACT_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
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InterPro; IPR004000; Actin_like.
Pfam; PF00022; Actin; 1.
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ses 15; Conserv
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                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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   Actin (Fragment)
                                                                                                                                                                  NCBI_TaxID=9542;
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CORTGEP
AC ORTGEP
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DT 01-JU
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DT 01-JU
DE ACTIN
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COC APOGA
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Hyla japonica (Japanese tree frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae; Hylinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Insocialization S., Kamishima Y., Iguchi T.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
-!-FUNCTION: Actina are highly conserved proteins that are involved in various types of cell motility and are ubiquitously expressed in all eukaryotic cells (By similarity).
-!-SIMILARITY: Belongs to the actin family.
EMBL; AB092520; BAC66208.1; -.
HSSP; PG0712; 1HLU.
GO; GO:0015629; C:actin cytoskeleton; IEA.
GO; GO:0015629; C:actin cytoskeleton; IEA.
InterPro; IPR004000; Actin_like.
Fram: PF00022; Actin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Hyloidea, Hylidae, Hylinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.

Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: Actins are highly conserved proteins that are involved in various types of cell motility and are ubiquitously expressed in all eukaryotic cells (By similarity).

-!- SIMILARITY: Belongs to the actin family.
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Pred. No. 1.1e-05;
; Mismatches 0; Indels
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                                                                                                                                                                                               01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Beta-actin 1 (Fragment)
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                                                                                                                                                       117 AA
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PROSITE; PS01132; ACTINS_ACT_LIKE; 1.
                                                                                                                                                       PRT;
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                                       91 TENTPAMYVAIQAVL 105
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1 TENTPAMYVAIQAVL 15
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Best Local Similarity 100.(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TFNTPAMYVAIQAVL
                                                                                                                                                                                                                                                                   Beta-actin 2 (Fragment).
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R HSSP, P60712; 1HLU.

R GO, GO: 0015629; C:actin cytoskeleton; IEA.

R GO, GO: 0015629; C:actin cytoskeleton; IEA.

R GO; GO: 0005200; F:structural constituent of cytoskeleton; IEA.

R InterPro; IPR004000; Actin_1:

R PRINTS; PR00130; ACTIN.

R PROSITE; P801132; ACTINS_ACT_LIKE; 1.

R Structural protein.

T NON TER 117 117

T NON_TER 117 117

T SEQUENCE 117 AA; 13291 MW, 64C6BAC4F84184CF CRC64;
                                                                                                                                                                                                           Query Match 100.0%; Score 74; DB 2; Length 117; Best Local Similarity 100.0%; Pred. No. 1.1e-05; Matches 15; Conservative 0; Mismatches 0; Indels
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Gaps

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Search completed: April 8, 2005, 12:03:09 Job time: 58.8667 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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April Run on:

8, 2005, 09:58:56; Search time 62.4 Seconds (without alignments) 92.971 Million cell updates/sec

US-09-423-351C-7 75

1 LPHAILRLDLAGRDL 15 score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 segs, 386760381 residues Searched:

2105692 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB : Maximum DB :

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

genesqp1980s:*
genesqp2000s:*
genesqp2000s:*
genesqp2001s:*
genesqp2001s:*
genesqp2003s:* A_Geneseq_16Dec04:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:*

# SUMMARIES

Description	Aaw92533 Beta-acti	Aam13687 Peptide #	Abb32618 Peptide #	Aam26087 Peptide #	7	9	Aam65825 Human bon	Aam53448 Human bra	Abg47471 Human liv	Aam01437 Peptide #		60	Aag26467 Arabidops		Abg15101 Novel hum	Abg15497 Novel hum	Human		Abm73899 DNA clone				Aag20916 Arabidops	Abu70549 Human adi	Aag50947 Arabidops
ID	AAW92533	AAM13687	ABB32618	AAM26087	ABB27467	ABB18116	AAM65825	AAM53448	ABG47471	AAM01437	ABG35459	AAG26468	AAG26467	ADK36534	ABG15101	ABG15497	ABP42912	ABU70816	ABM73899	AAG38700	AAG38699	AAG37992	AAG20916	ABU70549	AAG50947
DB	7	4	4	4	4	4	4	4	4,	4	ß	m	m	ß	4	4	ა	9	7	m	m	ო	'n	9	٣
Length DB	15	97	97	97	97	97	97	97	97	97	97	118	135	148	150	153	168	196	211	229	246	257	257	274	276
% Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
Score	75	75	75	75	75	75	75	75	75	75	75	75	75	75	75	75	75	75	75	75	75	75	75	75	75
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AAG05115 AAG20915 AAG3091 AD163068 AAG30914 AAG37990 AAG37290 AAG37210	AAGS0945 AAGS05113 AAG30774 AAG30774 AAG607390 AAG41511 AAG37317 AAG37317
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# ALIGNMENTS

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Peptide substrate, CCT, eukaryotic type II chaperonin complex; cyclin, binding agent; substrate-binding site; SBS; substrate folding; actin; tubulin; treatment; cancer; anticancer drug; viral infection; screening; reduced toxicity.
                                                 Beta-actin reference peptide substrate #7.
           AAW92533 standard; peptide; 15 AA
                                    (first entry)
                                    26-APR-1999
                       AAW92533;
RESULT 1
     AAW92533
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WO9853322-A1 Synthetic.

98WO-GB001485 22-MAY-1998; 26-NOV-1998.

97GB-00010762 23-MAY-1997;

(CANC-) INST CANCER RES ROYAL CANCER HOSPITAL.

Liou AK; Hynes G, Willison K,

WPI; 1999-070162/06.

Identifying specific binding agents for substrate binding site in CCT chaperonin complex - also new peptide binding agents and their mimetics, and peptides containing a specific CCT binding site, used for treating cancer

Disclosure; Fig 10; 97pp; English.

This invention describes a method which uses the CCT (eukaryotic type II chaperonin) complex or part of it, for identifying a binding agent that can occupy a substrate-binding site (SBS) on the CCT complex. By binding activity of the CCT complex, the binding agents block an SBS so that biological activity of the CCT complex is affected, particularly its ability to fold substrates such as actin, tubulin and cyclin. The binding agents are useful for treatment of cancer, particularly when used in combination with an anticancer drug, or viral infections. Nucleic acid fragments are used to screen for agents, e.g. binding agents that modulate interaction between the CCT complex and a protein that is to be folded. The binding

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells.
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                                                                                                                                                                                                                                                                                                                                                                                     Peptide #121 encoded by probe for measuring cervical gene expression.
                                                                                                                                               Gaps
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agents may target cells that are actively synthesising tubulin etc. Unlike known microtubule-stabilishing agents that affect all cells) should have reduced toxicity for normal cells. AAW92527-W92541 are peptide substrates used in the method of the invention
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                                                                                                                Length 15;
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30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
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27-SEP-2000; 2000US-0236359P
04-OCT-2000; 2000GB-00024263.
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                                                                                Seguence 15 AA;
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The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from MIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            exon nucleic acid probes useful for analyzing
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                                                                                                                                                                                            probe.
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                                                                                                                                                                                             Human; foetal liver; gene expression; single exon nucleic acid
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                                                                                                                                                                    Peptide #124 encoded by human foetal liver single exon probe.
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100.0%; Pred. No. 2.1e-06;
:ive 0; Mismatches 0;
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gene expression in human fetal liver
                                                                                         ABB32618 standard; peptide; 97 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chen W,
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2000US-0207456P
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Best Local Similarity
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26-MAY-2000;
30-JUN-2000;
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nucleic acid probes for measuring gene expression in a sample expression.

Trom human breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived probes with a collection of detectably labelled nucleic acids derived probe of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for determining predisposition and/or prognosing breast disease. Gene expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring gene expression, with far less bias than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence is a peptide concoded by a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed sequence in electronic format directly from WIPO
                                                                                                                                                                                                                             New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein #115 encoded by probe for measuring heart cell gene expression.
                                                                                                                                                                                                                                                                                                                                                              invention relates to a spatially-addressable set of single
                                                                                                                                                                                                                                                                                                                  Claim 27; SEQ ID NO 10435; 327pp + Sequence Listing; English.
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cardiovascular disease, hypertension, cardiac arrhythmia;
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                                                                                                                                             Chen W, Rank DR
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2000US-0207456P.
2000US-00608408.
2000US-00632366.
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27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
2000US-00632366
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congenital heart disease.
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26-MAY-2000; 2
30-JUN-2000; 2
03-AUG-2000; 2
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                   Probe; microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 27; SEQ ID NO 26356; 654pp; English.
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03-MG-2000; 2000US-00631346.
21-SEP-2000; 2000US-02346FPP.
27-SEP-2000; 2000US-023559P.
04-OCT-2000; 2000GB-00024263.
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26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-0060840B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human genetic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-488897/53
                                     genetic disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 97 AA;
                                                                                                                     WO200157272-A2
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                                                                               Homo sapiens.
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                                                                                                                                                                 09-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB27467;
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RESULT 5 ABB27467

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Gaps

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Length 97; 0; Indels

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                                                                                                                                         Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; bone marrow expressed exon; gene expression analysis; probe;
microarray; cancer; leukaemia; lymphoma; myeloma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human bone marrow expressed probe encoded protein SEQ ID NO: 26131,
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                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 75; DB 4; Length 97; 100.0%; Pred. No. 2.1e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                 Claim 15; SEQ ID NO 19886; 530pp; English.
                                                                                    Rank DR;
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                                                     (MOLE-) MOLECULAR DYNAMICS INC.
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                                                                                   Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MOLE-) MOLECULAR DYNAMICS INC
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
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2000US-0234687P.
2000US-0236359P.
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                                                                                   Hanzel DK,
                                                                                                             WPI; 2001-488899/53
                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
hes 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                           Sequence 97 AA;
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27-SEP-2000;
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Matches
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Chen W, Rank DR;

Hanzel DK,

Penn SG,

WPI; 2001-488900/53.

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                                                                                       The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention
              Human genome-derived single exon nucleic acid probes useful for analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of the probes of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human brain expressed single exon probe encoded protein SEQ ID NO: 25553.
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                                                                                                                                                                                                                                                                   Gaps
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                                                           Example 4; SEQ ID NO 26131; 658pp + Sequence Listing; English.
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                                                                                                                                                                                                                                      Length 97;
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                                                                                                                                                                                                                                 100.0%; Score 75; DB 4; 100.0%; Pred. No. 2.1e-06;
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                               gene expression in human bone marrow.
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26-MAY-2000; 2000US-0207456P.
30-UN-2000; 2000US-00608408.
303-AUG-2000; 2000US-0033366.
21-SEP-2000; 2000US-0234687P.
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Best Local Similarity 100.0%
Thes 15; Conservative
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                                                                                                                                                                                                      Sequence 97 AA;
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50 LPHAILRLDLAGRDL 64

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human adult liver.
                              Gaps
                                                                                                                                                                                                                                                                                                              Human, liver, cirrhosis, hyperlipoproteinaemia, hyperlipidaemia,
hypercholesterolaemia, coronary heart disease.
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Length 97;
                              Indels
100.0%; Score 75; DB 4; I 100.0%; Pred. No. 2.1e-06;
                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hanzel DK, Chen W, Rank DR;
                                                                                                                                                                                                                                                                               Human liver peptide, SEQ ID No 26119.
                                                                                                                                                                               ABG47471 standard; peptide; 97 AA
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30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
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                                                                 15
                                                                                  (first entry)
Query Match
Best Local Similarity 100.
Matches 15; Conservative
                                                               1 LPHAILRLDLAGRDL
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ABG47471
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The present invention relates to novel single exon nucleic acid probes (see AAI00010-AAI10067). The present sequence is a peptide encoded by one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic aetiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative breast diseases and non-carcinoma tumours. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel single exon nucleic acid probe used to measuring gene expression in
                                                                                                                                           Probe, human, breast disease, breast cancer, development disorder, inflammatory disease, proliferative breast disease, non-carcinoma tumour.
                                                                                                                  Peptide #119 encoded by probe for measuring human breast gene expression.
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100.0%; Pred. No. 2.1e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chen W, Rank DR
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                           AAM01437 standard; protein; 97
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2000US-00608408.
2000US-00632366.
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2000US-0236359P.
2000GB-00024263.
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                                                                                     (first entry)
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es 15; Conservative
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                                                                                                                                                                                                                       WO200157270-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a human breast.
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27-SEP-2000;
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RESULT 10
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0; Indels

100.0%; Score 75; DB 4; L 100.0%; Pred. No. 2.1e-06; tive 0; Mismatches 0;

Query Match
Best Local Similarity 100.
Matches 15; Conservative

Length 97;

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The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from thuman lung compirating single exon nucleic acid probes having one of 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614 probes. Also included are a microarray comprising the novel set of probes which hybridise at high stringency to a nucleic complements or the human lung; measuring gene expression in a sample derived from human lung; measuring gene expression in a sample acid expressed in the human lung; measuring gene expression in a sample collection of detectably labeled nucleic acids derived from human lung many; identifying exons in a eukaryotic genome, comprising (a) array; identifying exons in a eukaryotic genome, comprising (a) algorithmically predicting at least one exon from genomic sequences of the eukaryote; and (b) detecting specific hybridisation of detectably labeled nucleic acids from eukaryote lung mRNA, to a single exon probe, labeled nucleic acids from eukaryote lung mRNA, to a single exon probe, having a fragment identical to the predicted exon, the probe is included in the above mentioned microarray; assigning exons in several comprising (a) identifying exons from genomic sequence by the method above and (b) measuring the expression of each of the exons in the tissues and/or cell types using hybridisation to a single gene, comprising (c) in the exons in the tissues and/or cell types using hybridisation to a single sens of exons to exorate hypersession of the exons in the tissues and/or cell types using hybridisation. Or encoded by the exons should be assigned to a single gene in a peptide comprising one of 12011 sequences, mentioned in the specification, or encoded by the probes open reading frames (ORF). The probes are used for gene expression analyses, and for identifying exons in a gene, particularly using human lung derived mRNA and for the study of lung disea
                                                              Human peptide encoded by genome-derived single exon probe SEQ ID 25124.
                                                                          chronic observative bulmonary disease; interstitial lung disease; tamilial idiopathic pulmonary disease; interstitial lung disease; tuberous coleronte pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; daucher's disease, Nieman-Pick disease; Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; primary ciliary dyskinesis; pulmonary hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Spatially-addressable set of single exon nucleic acid probes, used to
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21-SEP-2000; 2000US-0234687P.
7-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
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2000US-00608408,
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                   (first entry)
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30-JUN-2000;
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                   19-AUG-2002
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histiocytosis, lymphangioleiomyomtosis, pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary dyskinesis, pulmonary hypertension and hyaline membrane disease. The present sequence is a peptide/protein encoded by a single exon probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                            Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
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                                                                                                                   100.0%; Score 75; DB 5; Length 97; 100.0%; Pred. No. 2.1e-06; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana protein fragment SEQ ID NO: 30934.
                                                                                                                                                                                                                                                  AAG26468 standard; protein; 118 AA.
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99US-0126264P.
99US-012678EP.
99US-0128234P.
99US-0128714AP.
99US-0130077P.
99US-0130077P.
99US-013049P.
99US-0131449P.
99US-0132484P.
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99US-0134941P.
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es 15; Conserv
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24-MAY-1999;
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16-SEP-1999; 20-SEP-1999; 22-SEP-1999; 23-SEP-1999; 24-SEP-1999; 28-SEP-1999;

04-0CT-1999 06-0CT-1999 06-0CT-1999 13-0CT-1999 13-0CT-1999 14-0CT-1999 14-0CT-1999 14-0CT-1999 14-0CT-1999 14-0CT-1999 16-0CT-1999 17-0CT-1999 18-0CT-1999 18-0C

us-09-423-351c-7.rag

99US-0147038P

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9905-0139452P

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9905-014433P

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06-AUG-1999;
06-AUG-1999;
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                                                           Length 118;
                                                       Query Match 100.0%; Score 75; DB 3; Length 11 Best Local Similarity 100.0%; Pred. No. 2.7e-06; Matches 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana protein fragment SEQ ID NO: 30933.
                                                                                                                                                                                                                                                                             AAG26467 standard; protein; 135 AA.
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99US-0123180P

99US-0125788P

99US-0126264P

99US-0127462P

99US-0127462P

99US-0128234P

99US-0128234P

99US-01308717P

99US-01308718P

99US-013081P

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990S-0137222P.
990S-0137228P.
990S-0137228P.
99US-0161993P.
99US-0162142P.
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                                                                                                                                      1 LPHAILRLDLAGRDL 15
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28-OCT-1999;
29-OCT-1999;
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05-MAR-1999;
23-MAR-1999;
25-MAR-1999;
25-MAR-1999;
01-APR-1999;
01-APR-1999;
06-APR-1999;
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30-APR-1999;
04-MAY-1999;
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04-JUN-1999;
07-JUN-1999;
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ID AAG26467

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This invention relates to a novel isolated polynucleotide comprising a nucleotide sequence selected from one of 1680 sequences, a mature protein coding portion of them, an active domain of them and their complementary sequences. The invention may be useful for the production of compounds with an antiarthritic, antiparkinsonian, neuroprotective, noctropic, immunosuppressive, cytostatic, antipsoriatic, antiparasitic activity. In antibacterial, antiviral, antifungal or antiparasitic activity. In addition, the disclosed sequences may be useful for gene therapy. The polypeptides or their antibodies are useful for treating many diseases such as arthritis, Parkinson's, Alzheimer's, autoimmune diseases, cancer, psoriasis, inflammatory bowel disease and infections caused by bacteria, viruses, fundi or parasites. The present sequence is that of a human polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated polynucleotide encoding bone marrow derived polypeptides useful for treating, e.g., Parkinson's, Alzheimer's, cancer, arthritis, Crohn's disease, and inflammatory bowel disease.
                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
1. .148
/label= OTHER
/note= "OTHER= All Xaa's in this sequence are unknown amino acids or the site of a stop codon within the DNA
                                                                                                                                                                                                                    antiarthritic; antiparkinsonian; neuroprotective; nootropic; immunosuppressive; cytostatic; antipsoriatic; antiinflammatory; antibacterial; antiviral; antifungal; antiparasitic; gene therapy; arthritis; Parkinson's; Alzheimer's; autoimmune disease; cancer; psoriasis; inflammatory bowel disease; infection; bacteria; virus; fungus; parasite; human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 20; SEQ ID NO 8616; 504pp; English.
                                                                                                   ADK36534 standard; protein; 148 AA.
                                                                                                                                                                                          Novel human polypeptide SeqID8616
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19-MAY-2000; 2000US-00574454
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1 LPHAILRLDLAGRDL 15
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                                                                                                                                                            06-MAY-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence"
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1es 15; Conservative
               WPI; 2002-280918/32.
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Misc-difference
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100.0%; Pred. No. 3.1e-06;
ive 0; Mismatches 0;
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99US-0147493P
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13-AUG-1999;
16-AUG-1999;
17-AUG-1999;
18-AUG-1999;
20-AUG-1999;
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23-AUG-1999;
23-AUG-1999;
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25-OCT-1999;
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Matches 15,
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12-OCT-15
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13-0CT-19
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Indels

Local Similarity 100

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The invention relates to isolated polymuclectide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PGR) primers, ollgomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymuclectides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal crivity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymuclectide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic pattent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at (ftp. WIPO.int/pub/published_pot_sequences)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                       Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                                                                                                                                 Novel human diagnostic protein #15092.
                                                                                                                ABG15101 standard; protein; 150 AA
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23-AUG-2000; 2000US-00649167.
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30 LPHAILRLDLAGRDL 44
                                                                                                                                                                                             (first entry)
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N-PSDB; AAS79288.
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100.0%; Score 75; DB 4; Length 150; 100.0%; Pred. No. 3.6e-06; ive 0; Mismatches 0; Indels

1 LPHAILRLDLAGRDL 15

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Local Similarity 100.

Query Match Best Loca Matches

Sequence 150 AA;

Search completed: April 8, 2005, 10:50:46 Job time : 63.4 secs

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Sequence 6, Appli
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Sequence 9424, Ap
Sequence 11313, A
Sequence 10409, A
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6100, Ap
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77, Appl
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                                                                                                                                                                                         (without alignments)
63.863 Million cell updates/sec
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/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                    GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-976-594-731
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US-09-949-016-110409
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Listing first 45 summaries
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Maximum DB seq length: 200000000
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28 55 73.3 394 4 US-09-949-016-6655 Sequence 6555, Ap 29 55 73.3 406 4 US-09-949-016-7396 Sequence 7396, Ap 31 46 66.7 336 4 US-09-248-796A-14108 Sequence 7396, Ap 31 46 61.3 670 4 US-09-228-991A-29837 Sequence 22079, Ap 32 45 60.0 327 4 US-09-222-991A-29837 Sequence 22079, Ap 34 41 54.7 354 4 US-09-222-991A-24162 Sequence 24162, Ap 35 41 54.7 354 4 US-09-222-991A-2142 Sequence 18669, Ap 36 41 54.7 354 4 US-09-222-991A-2162 Sequence 18669, Ap 37 41 54.7 354 4 US-09-252-991A-20697 Sequence 20697, Ap 38 41 54.7 354 4 US-09-252-991A-20697 Sequence 20697, Ap 38 41 54.7 354 4 US-09-252-991A-20697 Sequence 20697, Ap 38 41 54.7 354 4 US-09-252-991A-20697 Sequence 20697, Ap 38 41 54.7 354 4 US-09-252-991A-21032 Sequence 21032, Ap 38 52.0 182 4 US-09-252-991A-3164 Sequence 21032, Ap 41 40 53.3 3180 4 US-09-252-991A-3164 Sequence 21045, Ap 42 39 52.0 182 4 US-09-252-991A-30514 Sequence 2393, Ap 44 39 52.0 187 4 US-09-252-991A-30514 Sequence 30514, Ap 45 39 52.0 187 4 US-09-252-991A-30514 Sequence 30514, Ap 45 39 52.0 187 4 US-09-252-991A-30514 Sequence 35, App11
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### ALIGNMENTS

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US-09-306-446C.

| Sequence 5, Application US/09306446C
| Patent No. 4572959
| REGENERAL INFORMATION:
| APPLICANT: KIM, Dang Soo | APPLICANT: NAM, YOON Koon | APPLICANT: NAM, YOON WAN | APPLICANT: NAM, YOON | APPLICANT: Steen | No. 6087398e1 Sickle Cell Anemia Treatment | TITLE OF INVANTATION | No. 6087398e1 Sickle Cell Anemia Treatment | TITLE OF INVANTANT: Steen | APPLICANT: Steen | APPLICANT
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Gaps

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Indels

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Mismatches

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15; Conservative
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    Matches
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APPLICANT: KIM, Chul Geun
APPLICANT: KIM, Chul Geun
APPLICANT: KIM, Wan
APPLICANT: NOH, Jae Koo
APPLICANT: NOH, Jae Koo
APPLICANT: CHO, Kyou Nam
TITLE OF INVENTION: EXPRESSION VECTOR OF MUD LOACH GROWTH HORMONE GENE
FILE REFERENCE: P663144US0/Bas
CURRENT APPLICATION NUMBER: US/09/306,446C
CURRENT FILING DATE: 1999-05-06
PRIOR PILING DATE: 1998-06-01
NUMBER OF SEQ ID NOS: 33
SOOFTWARE: Patentin Ver. 2.0
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COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word for Macintosh
CURRENT APPLICATION DATA:
                                                                       APPLICATION NUMBER: US/08/609,236
FILING DATE: March 1, 1996
CLASSIFICATION: 514
PRIOR APPLICATION 514
PRIOR APPLICATION DATE:
APPLICATION NUMBER: 60/002,288
FILING DATE: August 14, 1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Benjamin Aaron Adler, Ph.D.
REGISTRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D5807
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-777-2321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/09306446C Patent No. 6372959
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ORGANISM: Misgurnus mizolepus
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SEQUENCE CHARACTERISTICS:
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Matches 15, Conservative
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DESCRIPTION: Protein
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DEVELOPMENTAL STAGE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
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TOPOLOGY: Linear
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ORIGINAL SOURCE:
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LENGTH: 374
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Query Match Best Local Similarity

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Furness, Michael
APPLICANT: Buchbinder, Jenny
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
FILE REFERENCE: PA-0641 US
CURRENT APPLICATION NUMBER: US/09/976,594
CURRENT FILING DATE: 2001-10-12
RIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 1143
SOFTWARE: PERL Program
SEQ ID NO 731
LENGTH: 375
TYPE: PRT
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                                                                                                                                                    VENDULY WESOULT WARRINGTON TO SOURCE TO SEQUENCE 14, Application US/08494151

Sequence 14, Application US/08494151

Sequence 14, Application US/08494151

SEQUENCE NO. SEGUENCE SEGUENCE SEGUENCE TRANSFORMATION:

TITLE OF INVENTION:

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Morison & Foerster STREET: 2000 Pennsylvania Ave. N.W., Suite 5500

CITY: Washington, D.C.

COUNTRY: USA

ZIP: 20006-1812

COMPUTER READBLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Is PROME PC Compatible

OPERATING SYSTEM: PC-DOS/NS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/494,151

FILING DATE: 23-JUN-1995

CLASSIFTCATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: MULASHING- KATE H.

REFERENCE/DOCKET NUMBER: 29,959

TELEFRANCE/LOCKET NUMBER: 29,959

TELEFRANCE/LOCKET NUMBER: 29,959

TELEFRANCE/LOCKET NUMBER: 20,030.01

TELEFRANCE (202) 887-1500

TELEFRANCE (202) 887-1500
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; Patent No. 6673549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           171 LPHAILRLDLAGRDL 185
                                                 171 LPHAILRLDLAGRDL 185
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1 LPHAILRLDLAGRDL 15
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US-09-949-016-10409
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Sequence 11313, Application US/09949016

Sequence 11313, Application US/09949016

GENERAL INFORMATION:

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTUMEN: PRESEQ FOR Windows Version 4.0

LENGTH: 404
                                                                                                                                                                                                                                                                                                                                                                                 Sequence 9424, Application US/09949016

Sequence 9424, Application US/09949016

Patent No. 681239

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOOL307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FASESO FOR WINDOWS VERSION 4.0

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                                                                                                                                 100.0%; Score 75; DB 4; Length 375; 100.0%; Pred. No. 7.7e-06; ive 0; Mismatches 0; Indels
                                         ; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 1837317CD1
US-09-976-594-731
                                                                                                                                                                                                                                                                 195 LPHAILRLDLAGRDL 209
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Best Local Similarity 100.0°
Matches 15; Conservative
                                                                                                                                 Query Match 100.
Best Local Similarity 100.
Matches 15; Conservative
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-949-016-11313
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US-09-949-016-9424
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WS-09-949-016-10409

Sequence 10409, Application US/09949016

Patence 10409, Application US/09949016

Patence 10409, Application US/09949016

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR PILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-010-03

SEQ ID NOS: 207012

SEQ ID NO 10409

SEQ ID NO 10409
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| Sequence 16, Application US/09106217
| Patent No. 606356
| GENERAL INFORMATION: A PAPLICANT Keating Mark T. | APPLICANT Olson, Timothy M. | TITLE OF INVENTION: Actin Mutations in Dilated | TITLE OF INVENTION: Cardiomyopathy, a Heritable Form of Heart Failure | TITLE OF INVENTION: Cardiomyopathy, a Heritable Form of Heart Failure | STREET OF SEQUENCES: 18 | CORRESPONDENCE ADDRESS: ADDRESSER: Rothwell, Figg, Ernst & Kurz, P.C. | STREET: Tower | STREET: Tower | STREET: Tower | STREET: Tower | STREET: Down | STATE: DC | COUNTRY: U.S.A. | COUNTRY
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                                                                                                Gaps
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     Length 404;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97.3%; Score 73; DB 4; 1
93.3%; Pred. No. 1.1e-05;
                                                                                           0; Mismatches
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APPLICATION NUMBER: US/09/106,217
Query Match
Best Local Similarity 100.0%;
Matches 15; Conservative 0
                                                                                                                                                                                                                                                                                        200 LPHAILRIDLAGRDL 214
                                                                                                                                                                                                 1 LPHAILRLDLAGRDL 15
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ATTORNEY/AGENT INFORMATION:
NAME: Saxe, Stephen A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:

APPLICANT: MCHUGH, KITK M.

TITLE OF INVENTION: MALIGNANCY OF SMOOTH MUSCLE TUMORS

TITLE OF INVENTION: MALIGNANCY OF SMOOTH MUSCLE TUMORS

TUTLE OF INVENTION: MALIGNANCY OF SMOOTH MUSCLE TUMORS

TOTLE OF INVENTION: MALIGNANCY OF SMOOTH MUSCLE TUMORS

CORRESPONDENCES:

ADDRESSEE: Moodcock Washburn Kurtz Mackiewicz &

ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &

ADDRESSEE: Woodcock Washburn Kurtz Packiewicz &

GITY: Philadelphia
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STATE: PA
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/588,113
RECISTRATION NUMBER: 38,609
REFERENCE/DOCKET NUMBER: 2323-125
FELECOMMUNICATION INPORMATION:
TELEPRAK: 202-783-6040
FELEFAX: 202-783-6031
INPORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: JINEAR
SECULE TYPE: protein
US-09-106-217-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION: 436
ATCHNEY/AGENT INFORMATION:
NAME: Ralph, Rebecca L.
REGISTRATION NUMBER: 35,152
REFERENCE/DOCKET NUMBER: TJU-1
TELECOMMUNICATION INFORMATION:
TELEFAX: 215-568-3100
TELEFAX: 215-568-3100
TELEFAX: 215-568-3100
TELEFAX: 215-568-3100
TELEFAX: 215-568-3100
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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Patent No. 5710003
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172 LPHAIMRLDLAGRDL 186
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Best Local Similarity 93.3
Matches 14; Conservative
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MOLECULE TYPE: protein
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RESULT 11

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Generate 6.021, Application US/09949016

APPLICANT VERTER, J. Craig et al.

TITLE 0F INVESTION: WITH HUMAN DISEASE, WETHORS OF DETECTION AND USES THEREOF TITLE 0F INVESTION: WITH HUMAN DISEASE, WETHORS OF DETECTION AND USES THEREOF CREEK PREDICATION WITH HUMAN DISEASE, WETHORS OF DETECTION AND USES THEREOF CREEK PREDICATION WINNERS: 60/121, 49

FILES OF PRICEATION WITH ADMINISTRATION (20/121, 76)

FRIEND FILEND ANTE: 2000-10-10

SERVINE PRICEATION WITH ADMINISTRATION (20/121, 76)

FRIEND FILEND ANTE: 2000-10-10

SERVINES OF SEQUENCY WINNERS: 60/121, 76

FRIEND APPLICANT SEALING WINNERS: 10/121, 76

FRIED APPLICANT SEALING WINNERS: 10/121, 76

FRIED APPLICANT SEALING WINNERS: 10/121, 76

FRIED APPLICANT SEALING FOR APPLICANT SEALING
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Search completed: April 8, 2005, 12:07:36 Job time : 17.5333 secs
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APPLICANT: VEWTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REPRENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,756
PRIOR PILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTHARE: PRESEEC for Windows Version 4.0
SEQ ID NO 7721
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APPLICANT: Mutter, Jan
TITLE OF INVENTION: Prognostic Classification of Breast Cancer
TITLE OF INVENTION: Prognostic Classification of Breast Cancer
FILE REFERENCE: B0801/7224 (JRV)
CURRENT APPLICATION NUMBER: US/09/917,254
PRIOR APPLICATION NUMBER: US 60/222,093
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 102
SOFTWARE: Patentin version 3.0
SEQ ID NO 53
LENGTH: 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 97.3%; Score 73; DB 4; Length 377; Best Local Similarity 93.3%; Pred. No. 1.8e-05; Matches 14; Conservative 1; Mismatches 0; Indels
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                                           Length 377;
                                                                                  0; Indels
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Pred. No. 1.9e-05;
1; Mismatches 0;
                                         97.3%; Score 73; DB 3; 193.3%; Pred. No. 1.8e-05; tive 1; Mismatches 0
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; Patent No. 6812339
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; Sequence 53, Application US/09917254
; Patent No. 6703204
; GENERAL INFORMATION:
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173 LPHAIMRLDLAGRDL 187
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                              Ouery Match
Best Local Similarity 93.3<sup>3</sup>
Matches 14; Conservative
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Best Local Similarity 93.3
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7721
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US-09-949-016-7721
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US-09-106-217-2
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Sequence 10757, Application US/09949016

Betent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
FRIOR APPLICATION NUMBER: 00/241,755
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR PILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-10-08
SOFTWARE: FASEESQ for Windows Version 4.0
SEQ ID NO 10757
LENGTH: 402
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93.3%; Pred. No. 2e-05;
iive 1; Mismatches
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Best Local Similarity 93.34
Matches 14; Conservative
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ORGANISM: Human
US-09-949-016-10757
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April 8, 2005, 10:53:18 ; Search time 42.6667 Seconds (without alignments) 116.718 Million cell updates/sec
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3: /cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
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7: /cgn2_6/ptodata/1/pubpaa/USO8_BWPUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/USO8_BWPUB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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1 LPHAILRLDLAGRDL 15
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Maximum DB seq length: 200000000
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## SUMMARIES

	Description	Sequence 214884,	Sequence 33414, A	Sequence 175571,	Sequence 4044, Ap	Sequence 169247,	Sequence 56, Appl	Sequence 42770, A	Sequence 206389,	Sequence 162706,	Sequence 43575, A	Sequence 44494, A	Sequence 69353, A	Sequence 177530,
	ΠD	US-10-424-599-214884	US-09-864-761-33414	US-10-424-599-175571	US-10-264-049-4044	US-10-437-963-169247	US-10-002-631C-56	US-10-767-701-42770	US-10-424-599-206389	US-10-437-963-162706	US-10-767-701-43575	US-10-425-114-44494	US-10-425-114-69353	US-10-424-599-177530
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	Query Match Length DB	44	97	156	168	180	219	230	236	238	249	250	254	261
de	Query	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
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RESULT 2 US-09-864-761-33414 S-09-864-761-33414, Application US/09864761 ; Patent No. US20020048763A1

Sequence 52089, A Sequence 57500, A Sequence 278431, Sequence 59172, A Sequence 591333, Sequence 88, Appl Sequence 97, Appl Sequence 179917, Sequence 202420, Sequence 52, Appl Sequence 162000, A Sequence 52, Appl Sequence 52, Appl Sequence 162009, Sequence 162085, Sequence 162086, Sequence 162085, Sequence 162085, Sequence 2233492, Sequence 233345, Sequence 233335, Sequence 233335, Sequence 233345, Sequence 2333345, Sequence 233345, Sequence 2333335, Sequence 2333345, Sequence 2333335, Sequence 2333335, Sequence 2333335, Sequence 2333335, Sequence 2333335, Sequence 2333335, Sequence 2	0 11 11 11 11 11 11 11 11
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#### ALIGNMENTS

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Sequence 214884, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; GENERAL INFORMATION:
; APPLICANT: La Nosa Thomas J
; APPLICANT: Covalic David K
; APPLICANT: Cao Yongway Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: VIDIATE: US/10/424,599
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 214884
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US-10-424-599-214884
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Similarity 100.0%; Pred. No. 8.8e-06;
15; Conservative 0; Mismatches 0;
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US-10-424-599-214884
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Best Local Simil
Matches 15;
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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
ENGY ID NO 175571
LENGTH: 156
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Sequence 4044, Application US/10264049

Publication No. US20040005579A1

GENERAL INFORMATION:

APPLICANT: Birse et al.

TITLE OF INFORMATION:

CURRENT APPLICATION NUMBER: US/10/264,049

CURRENT FILING DATE: 2002-10-04

PRIOR APPLICATION NUMBER: DET/US01/18569

PRIOR APPLICATION NUMBER: US 60/209,467

PRIOR PILING DATE: 2001-06-07

NUMBER OF SEQ ID NOS: 4360

SOFTWARE: Patentin Ver. 3.1

SEQ ID NO 4044
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 156;
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; OTHER INFORMATION: Clone ID: PAT_MRT3847_129559C.1.pep
US-10-424-599-175571
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
100.0%; Score 75; DB 15;
Best Local Similarity 100.0%; Pred. No. 3.5e-05;
Matches 15; Conservative 0; Mismatches 0;
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                                                                                                         Sequence 175571, Application US/10424599; Publication No. US20040031072A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-437-963-169247; Sequence 169247, Application US/10437963; Publication No. US20040123343A1; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34 LPHAILRLDLAGRDL 48
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                  57 LPHAILRLDLAGRDL 71
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US-10-264-049-4044
                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                               US-10-424-599-175571
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ORGANISM:
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ò
 N: EXPRESSED IN HEART, SIGNAL = 48

N: EXPRESSED IN BONE MARROW, SIGNAL = 81

N: EXPRESSED IN ADULT LIVER, SIGNAL = 28

N: EXPRESSED IN PLACENTA, SIGNAL = 24

N: EXPRESSED IN PLACENTA, SIGNAL = 37

N: EXPRESSED IN HEL100, SIGNAL = 78

N: EXPRESSED IN FETAL LIVER, SIGNAL = 45

N: EXPRESSED IN HELA, SIGNAL = 45

N: EXPRESSED IN HELA, SIGNAL = 40

N: EXPRESSED IN HELA, SIGNAL = 40

N: EXTHUMAN HIT: BE2171730.1, EVALUE 3.00e-50

N: WISSEROT HIT: 042161, EVALUE 4.00e-51

N: EXT_HUMAN HIT: BE256272.1, EVALUE 4.00e-50
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HFART, SIGNAL = 48
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Best Local Similarity 100.
Matches 15, Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: E                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION:
OTHER INFORMATION:
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Gaps

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APPLICANT: Evaluation of the state of the st
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| Sequence 206389, Application US/10424599
| Sequence 206389, Application US/10424599
| Publication No. US20040031072A1
| GENERAL INFORMATION:
| APPLICANT: La Rosa Thomas J
| APPLICANT: Cao Yongwei
| TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement TITLE OF INVENTION: 18/10/424,599
| CURRENT APPLICATION NUMBER: US/10/424,599
| CURRENT PILING DATE: 2003-04-28
| NUMBER OF SEQ ID NOS: 288684
| SEQ ID NO 206389
| LENGTH: 236
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                                                                                                                                                                                                                                                                                                                                         Length 230;
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                                                                                                                                                                                                                                           ; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C17410_1.pep
US-10-767-701-42770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Clone ID: PAT_MRT3847_28396C.1.pep
US-10-424-599-206389
                                                                                                                                                                                                                                                                                                                                             Score 75; DB 16;
Pred. No. 5.4e-05;
; Mismatches 0;
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OTHER INFORMATION: unsure at all Xaa locations
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Best Local Similarity 100.0%;
Matches 15; Conservative 0
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Best Local Similarity 100.0%;
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                                      NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 42770
LENGTH: 230
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ORGANISM: Sorghum bicolor
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Glycine max
          CURRENT FILING DATE:
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                                                                                                                                                                                                                                    APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21 (53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 169247
LENGTH: 180
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Publication No. US20040172684A1
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
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US-10-02-631C-56
US-10-02-65, Application US/10002631C
Publication No. US20030157486A1
GENERAL INPORMATION:
APPLICANT: Graff, Jonathon M.
APPLICANT: Muenter, Matthew
TILLE OF INVENTION: METHODS TO IDENTIFY SIGNAL SEQUENCES
FILE REFERENCE: A34943 090495.0243
CURRENT FILING DATE: 2001-10-31
PRIOR PLILING DATE: 2001-10-31
PRIOR PLILING DATE: 2001-6-21
NUMBER OF SEQ ID NOS: 324
SOFUTARE: PSELSEQ for Windows Version 4.0
SEQ ID NO 56
LENGTH: 219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Clone ID: PAT_MRT4530_67685C.1.pep
US-10-437-963-169247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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La Rosa, Thomas J.
Kovalic, David K.
Zhou, Yihua
Cao, Yongwei
Wu, Wei
Boukharov, Andrey A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         198 LPHAILRIDLAGRDL 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 LPHAILRLDLAGRDL 15
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Matches 15; Conservative
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nes 15; Conservative
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ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Homo sapiens
US-10-002-631C-56
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ORGANISM: Glycine max
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US-10-4494

i Sequence 44494, Application US/10425114

j Sequence 44494, Application US/10425114

j Publication No. US2004003488A1

j PublicANT: Liu, Jingdong

j APPLICANT: Liu, Jingdong

j APPLICANT: Screen, Steven E

j APPLICANT: Tabaska, Jack E

j APPLICANT: Pabaska, Jack E

j APPLICANT: Pabaska, Jack E

j APPLICANT: Pabaska, Jack E

j APPLICANT: Screen, Steven 
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Westor 10

Westor 10

Sequence 43575, Application US/10767701

Sequence 43575, Application US/10767701

Sequence 43575, Application Westor 10

Sequence 43575, Application Westor 10

Sequence 43575, Application Westor 10

Septicant: Cao, Yinua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Number and Uses Thereof For Plant Improvement

FILE REFERENCE: 30-21 (53355)

CURRENT FILING DATE: 2004-01-29

NUMBER OF SEQ ID NOS: 63128

SEQ ID NO 43575

LENGTH: 249
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100.0%; Score 75; DB 16; Length 238;
Best Local Similarity 100.0%; Pred. No. 5.6e-05;
Matches 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 75; DB 16; Length 249; 100.0%; Pred. No. 5.9e-05;
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US-10-767-701-43575
                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Clone ID: PAT_MRT4530_61772C.1.pep
US-10-437-963-162706
                                                                                                                                                                                                                                  NAME/KEY: unsure
LOCATION: (1)..(238)
OTHER INFORMATION: unsure at all Xaa locations
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NUMBER OF SEQ ID NOS: 204966
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Best Local Similarity 100...
Local Similarity 100...
Local Similarity 100...
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ORGANISM: Sorghum bicolor
                                                                                                                                                          ORGANISM: Oryza sativa
                                     SEQ ID NO 162706
LENGTH: 238
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Sequence 69353, Application US/10425114

Publication No. US20040034888A1

GENERAL INFORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Elou, Yihua

APPLICANT: Elou, Yihua

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE SEFRENCE: 38-21(53313)B

CURRENT APLICATION NUMBER: US/10/425,114

CURRENT PILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NO 69353

LENGTH: 254
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Publication No. US20040031072A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Acoustic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Sy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 17530
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                                                                             Length 250;
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; OTHER INFORMATION: Clone ID: PAT_MRT3847_131325C.1.pep
US-10-424-599-177530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Clone ID: UC-ZMFLB73022E07_FLI.pep
US-10-425-114-69353
                                                                          Score 75; DB 15;
Pred. No. 5.9e-05;
; Mismatches 0;
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; OTHER INFORMATION: Clone ID: 700978095_FLI.pep
US-10-425-114-44494
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                                                                          Query Match

Best Local Similarity 100.0%;

Matches 15; Conservative 0
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Rest Local Similarity 100...
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ORGANISM: Glycine max
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Best Local Similarity
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Sequence 5750. Application US/10425114
; Sequence 5750. Application No. US20040034888A1
; Publication No. US2004003488BA1
; Publication No. US2004003488BA1
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; RUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 57500
; SEQ ID NO 57500
                                                                                                                                                                                                                                                                                                                  APPLICANT: Liu, vinguous
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Labatka and Uses Thereof for Plant Improvement
FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313) B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 52089
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100.0%; Score 75; DB 15; Length 288;
Best Local Similarity 100.0%; Pred. No. 6.9e-05;
Matches 15; Conservative 0; Mismatches 0; Indels
0; Indels
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US-10-425-114-57500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Clone ID: 701149157_FLI.pep
US-10-425-114-52089
0; Mismatches
                                                                                                                                                                                              US-10-425-114-52089
; Sequence 52089, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
                                                  1 LPHAILRLDLAGRDL 15
                                                                       1 LPHAILRLDLAGRDL 15
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15; Conservative
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ORGANISM: Glycine max
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ORGANISM: Zea mays
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Matches
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OM protein - protein search, using sw model

April 8, 2005, 09:58:56; Search time 9.3333 Seconds Run on:

(without alignments)
154.634 Million cell updates/sec

US-09-423-351C-7 75 1 LPHAILRLDLAGRDL 15 Perfect score:

Scoring table: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:* Database :

1: pirl:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	- Cali		actin homolog prot		beta	actin 2 - Arabidop	ţ	ω		actin beta - bovin	ı			_	actin - Acanthamoe	_	actin - slime mold		actin gamma 1 - hu		actin gamma - mous	actin beta, non-mu	- maize	gamma, c	beta-	actin beta-1, cyto	actin beta, cytoso	actin beta - goose	actin - Puccinia g
SUMMARIES	ΩĪ	A31409	S20097	JC2008	S11452	S05430	S68089	A26559	368090	A29664	ATBOB	ATBOG	JC5818	ATRTC	A48324	ATAX	ATCHB	ATDO	ATHUB	ATHUG	ATMSB	ATMSG	ATRBB	ATZM1	S11222	S71125	S71124	S71126	A55001	842103
	Length DB	92		325 2					362 2	••	•	•	374 2	375 1	375 1	375 1	375 1	375 1	375 1	375 1	375 1	375 1	375 1	375 1		•	•	•	375 2	•
de	Query Match		100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
	Score	75	75	75	75	75	75	75	75	75	75	75	75	75	75	75	75	75	75	75	75	75	75	75	75	75	75	75	75	75
	Result No.		~	m	4	2	9	7	œ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

actin - Phaffia rh actin 7 - fruit fl actin - Soybean actin gamma, cytos actin - Entamoeba actin - B. Fuit fl actin - Sime mold actin - Sime mold actin - Sime mold actin 21 - sime Actin 12 - sime Actin 13 - nematod actin 12 - fruit actin - fruit	actin, cytosolic - actin, muscle - st actin 15A - sea ur
ST0377 ATFF7 ATS73 A43552 ATAXE ATAXE ATRF8 ATRF8 ATRZ3 ATRZ3 ATRZ3 ATRZ3 ATRZ3 AG8449	JS0189 JS0190 S07288
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277222222222222222222222222222222222222	75 75 75
0 11 0 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	. 4. 4. 4. 1 6. 4. 7.

#### ALIGNMENTS

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actin - California sea hare (fragments)
C;Species: Aplysia californica (California sea hare)
C;Species: Aplysia californica (California sea hare)
C;Species: Aplysia californica (California sea hare)
C;Accession: Al1409; A60977
R;Kennedy, T.E.; Gawinowicz, M.A.; Barzilai, A.; Kandel, B.R.; Sweatt, J.D.
Proc. Natl. Acad. Sci. U.S.A. 85, 7008-7012, 1998
A;Title: Sequencing of proteins from two-dimensional gels by using in situ digestion and tion in Aplysia.
A;Reference number: A94207; MUID:88320566; PMID:3413132
A;Accession: A1409
A;Molecule type: protein
A;Residuces: 1-18,21-92 cxEND-
A;Residuces: 1-18,21-92 cxEND-
A;Residuces: 1-18,21-92 cxEND-
A;Residuces: 1-18,21-92 cxEND-
A;Residuces: 1-18,15-197, 1899
B;Sweatt, J.D.; Kennedy, T.E.; Wager-Smith, K.; Gawinowicz, M.A.; Barzilai, A.; Karl, K
B;Sweatt, J.D.; Kennedy, T.E.; Wager-Smith, R.; Gawinowicz, M.A.; Barzilai, A.; Karl, K
B;Sweatt, J.D.; Kennedy, T.E.; Wager-Smith, R.; Gawinowicz, M.A.; Barzilai, A.; Karl, K
B;Sweatt, J.D.; Annedy, T.E.; Wager-Smith, R.; Gawinowicz, M.A.; Barzilai, A.; Karl, K
B;Sweatt, J.D.; A;Accession: A60977; MUID:89276264; PMID:2731514
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A, Molecule type: protein A, Residues: 1-20 <SWE> C, Superfamily: actin

ö Gaps ; 0 Length 92; 0; Indels 100.0%; Score 75; DB 2; I 100.0%; Pred. No. 9.5e-07; Mismatches . Conservative Best Local Similarity Matches 15; Conserv Query Match ò

# 1 LPHAILRLDLAGRDL 15 41 LPHAILRIDLAGRDL 55

셤

RESULT 2

actin 85c - potato (fragment)
C;Species: Solanum tuberosum (potato)
C;Species: Solanum tuberosum (potato)
C;Accession: 22-Nov-1993 #sequence_revision 17-Oct-1997 #text_change 09-Jul-2004
C;Accession: 820097
R;Drouin, G; Dover, G.A.
J Mol. Evol. 31, 132-150, 1990
A;Title: Independent gene evolution in the potato actin gene family demonstrated by phyl A;Reference number: 820092; MUID:91012599; PMID:2120451
A;Recession: 820097
A;Molecule type: DNA
A;Residues: 1-195 <DRO>
A;Residues: 1-195 <DRO>
A;Residues: 1-195 <DRO>
A;Cenetics: 1-195 <DRO>
A;Cenetics: 1-195 <DRO 820097

A,Introns: 132/1 C,Superfamily: actin C,Keywords: cytoskeleton; structural protein

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Gaps

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C;Accession: S68089
R;McDowell, J.M.; Huang, S.; McKinney, E.C.; An, Y.Q.; Meagher, R.B.
Genetics 142, 587-602, 1996
A;Title: Structure and evolution of the actin gene family in Arabidopsis thaliana.
A;Reference number: S68089; MUID:96188109; PMID:8852856
A;Recession: S68089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     actin type 5, cytosolic - chicken
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Accession: A26559
R;Bergsma, D.J; Chang, K.S.; Schwartz, R.J.
MOI. Cell. Biol. 5, 1151-1162, 1985
A;Reference number: A26559; MUID:85213487; PMID:4000121
A;Reference property Paragonal A26559; MUID:85213487; PMID:4000121
A;Reference number: A26559; MUID:85213487; PMID:4000121
A;Reference number: A26559; MUID:85213487; PMID:4000121
C;Superfamily: actin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 05-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
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; Pred. No. 4.5e-06;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                          100.0%; Score 75; DB 2; Length 328; 100.0%; Pred. No. 4.1e-06;
                                                                                                                                                                                     A; Introns: 41/3; 121/3; 268/1
C; Superfamily: actin
C;Keywords: cytoskeleton; methylated amino acid
F;73/Modified site: 3'-methylhistidine (His) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Reywords: cytosol; methylated amino acid
F;74/Modified site: 3'-methylhistidine (His) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: not compared with conceptual translation A;Molecule type: DNA A;Residues: 1-361 <MCD>
                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                               A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-328 <LIU>
A;Cross-references: UNIPROT:P83751; EMBL:M25013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: ACT2
C;Superfamily: actin
C;Keywords: cytoskeleton; structural protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: UNIPROT: 093ZL9
A; Note: mRNA sequencing was also done
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0%;
Matches 15; Conservative 0;
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Best Local Similarity 100.0
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                actin homolog protein - red swamp crayfish
C;Species: Procambarus clarkii (red swamp crayfish)
C;Species: Procambarus clarkii (red swamp crayfish)
C;Species: Procambarus clarkii (red swamp crayfish)
C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 20-Jun-2000
C;Accession: JC2008
R;Kang, W.K.; Naya, Y.
G;Accession: JC2008
A;Title: Sequence of the cDNA encoding an actin homolog in the crayfish Procumbarus clar A;Reference number: JC2008
A;Accession: JC2008
A;Coss-references: GB:D14612; NID:G434784; PIDN:BAA03463.1; PID:G434785
A;Experimental source: muscle
C;Superfamily: actin
C;Keywords: muscle contraction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S11452

S11452

actin (clone 302) - brine shrimp (fragment)
C,Species Atremia sp. (brine shrimp)
C;Species 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C;Accession: S11452
F,Macias M.T.; Sastre, L.
Nucleic Acids Res. 18, 5219-5225, 1990
A;Title: Molecular cloning and expression of four actin isoforms during Artemia developm A;Reference number: S11450; MUD:90384823; PMID:2402445
A,Reference number: S11450
A,Residues: 1-327 cMAC>
A,Residues: 1-327 cMAC>
A,Residues: 1-327 cMAC>
C;Superfamily: actin
C;Reywords: methylated amino acid; structural protein
C;Reywords: methylated amino acid; structural protein
C;Reywords: methylated acid site: 3'-methylhistidine (His) #status predicted
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C;Species: Ctenopharyngodon idella (grass carp)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004
C;Accession: S05430 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004
R;Liu, Z.; Zhu, Z.; Roberg, K.; Faras, A.J.; Guise, K.S.; Kapuscinski, A.R.; Hackett,
Nucleic Acids Res. 17, 5850, 1989
A;Title: The beta-actin gene of carp (Ctenopharyngodon idella).
A;Title: The beta-actin gene of carp (Ctenopharyngodon idella).
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100.0%; Score 75; DB 2; Length 195; 100.0%; Pred. No. 2.2e-06; Live 0; Mismatches 0; Indels
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                                                                                                                                                                        153 LPHAILRLDLAGRDL 167
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Matches 15, Conservative
   Query Match 100.
Best Local Similarity 100.
Matches 15; Conservative
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Best Local Similarity 100.
Matches 15; Conservative
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Gaps

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Gaps

RESULT 5 S05430

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A;Note: only peptides that differed in composition from the corresponding peptides of ra R;Degen, J.L.; Neubauer, M.G.; Degen, S.J.F.; Seyfried, C.E.; Morris, D.R. D.R. J. Bhol. Chem. 258, 12131-12162, 1983
A;Title: Regulation of protein synthesis in mitogen-activated bovine lymphocytes. Analys A;Reference number: A39105; MUID:84032385; PMID:6195151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Superfamily: actin
C;Keywords: blocked amino end; cell motility; cytoskeleton; methylated amino acid; micro
F;1/Modified site: blocked amino end (Asp) (probably acetylated) #status experimental
F;72/Modified site: 3'-methylhistidine (His) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Bos printgenius taurus (cattle)
C;Species: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: B14185; A02999
R;Vandekerckhove, J;Weber, K.
Bur. J. Biochem. 90, 451-462, 1978
Bur. J. Biochem. 90, 451-462, 1978
A;Title: Actin amino-acid sequences. Comparison of actins from calf thymus, bovine brain A;Reference number: A14185; MUID:79045349; PMID:213279
A;Accession: B14185
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C;Species: Homo sapiens (man)
C;Date: 20-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 09-Jul-2004
C;Date: 20-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 09-Jul-2004
C;Accession: JG5818; PC4501
R;Hauschildt, S.; Schwarz, C.; Heine, H.; Ulmer, A.J.; Flad, H.D.; Rietschell, B.T.; Jens Biochem. Biophys. Res. Commun. 241; 670-674, 1997
A;Title: Actin: A target of lipopolysaccharid-induced phosphorylation in human monocytes A;Reference number: JG5818; MUID:98096379; PMID:9434766
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A,Cross-references: UNIPROT:P02571
A,Cross-references: UNIPROT:P02571
C,Comment: valy peptides that differed in composition from the corresponding peptides of ra C,Comment: vertebrate nonmuscle cells contain two highly conserved cytoskeletal actins, C,Superfamily: actin
                                                                                                                                                                                                                                                                                                     A;Molecule type: mRNA
A;Residues: 76-227;344-374 <DEG>
A;Residues: 76-227;344-374 <DEG>
A;Cross-references: GB:K00622; GB:K00623
A;Note: actins beta and gamma were not distinguished in this study
C;Comment: Vertebrate nonmuscle cells contain two highly conserved cytoskeletal actins,
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Pred. No. 4.7e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        170 LPHAILRIDLAGRDL 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    170 LPHAILRLDLAGRDL 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 LPHAILRLDLAGRDL 15
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Best Local Similarity 100.
Matches 15; Conservative
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Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gamma-actin - human
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C;Species: Strongylocentrotus purpuratus (purple urchin)
C;Date: 15-Dec-1988 #sequence_revision 30-Sep-1991 #text_change 05-Dec-1997
C;Accession: A29664
R;Crain Jr., W.R.; Boshar, M.F.; Cooper, A.D.; Durica, D.S.; Nagy, A.; Steffen, D.
J. Mol. Evol. 25, 37-45, 1987
A;Title: The sequence of a sea urchin muscle actin gene suggests a gene conversion with A;Reference number: A29664; MUID:87311761; PMID:3114500
A;Accession: A29664
A;Molecule type: DNA
A;Residues: 1-370 ACRA>
A;Cross-references: GB:X05739; GB:X05740; GB:X05741; GB:X05742; GB:X05743
A;Cross-references: GB:X05739; GB:X05740; GB:X05741; GB:X05742; GB:X05743
C;Superfamily: actin
C;Superfamily: actin
C;Superfamily: actin
C;Keywords: methylated amino acid
F;73/Modified site: 3'-methylhistidine (His) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         defin beta - bovine (tentative sequence)

(species: Bos primiganius taurus (cattle)

(species: Bos primiganius taurus (cattle)

(species: 30-Sep-1991 #sequence revision 30-Sep-1991 #text_change 09-Jul-2004

(species: 30-Sep-1991 #sequence 130-5 #02999; A14185

R;Vandekerckhove, J; Weber, K.

R;Vandekerckhove, J; Webe
                                                                                                                                                actin 8 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Accession: S68090
C;Accession: S68090
R;McDowell, J.M.; Huang, S.; McKinney, E.C.; An, Y.Q.; Meagher, R.B.
Genetics 142, 587-602, 1996
A;Title: Structure and evolution of the actin gene family in Arabidopsis thaliana.
A;Reference number: S68089; MUID:96158109; PMID:8852856
A;Title: Structure and evolution of the actin gene family in Arabidopsis thaliana.
A;Reference number: S68089
A;Status: not compared with conceptual translation
A;Status: not compared with conceptual translation
A;Residues: 1-362 eMCD>
A;Cress-references: UNIPROT:08LB94
A;Note: mRNA sequencing was also done
C;Genetics:
A;Gene: ACTB
C;Superfamily: actin
C;Keywords: cytoskeleton; structural protein
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1 LPHAILRLDLAGRDL 15

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Local Similarity nes 15; Conserv

Best Loc Matches

Query Match

168 LPHAILRLDLAGRDL 182

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1 LPHAILRLDLAGRDL 15

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Conservative
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                  15;
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                  Matches
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actin beta, cytoskeletal - common carp
C;Species Cyprinus carpio (common carp)
C;Species Cyprinus carpio (common carp)
C;Accession: A48324 #sequence_revision 11-Apr-1997 #text_change 09-Jul-2004
C;Accession: A48324
C;Accession: A48324
DNA Seq. 1, 125-136, 1990
A;Title: Isolation and characterization of beta-actin gene of carp (Cyprinus carpio).
A;Title: Isolation and characterization of beta-actin gene of carp (Cyprinus carpio).
A;Reference number: A48324; MUID:92190540; PMID:2134183
A;Residues: 1-375 < LIU>
A;Residues: 1-375 < LIU>
A;Residues: 1-375 < LIU>
A;Residues: Learned number: Akino Ciprinus carpio).
A;Residues: Learned number: Akino Ciprinus carpio).
A;Residues: Learned carpidation carpio Ciprinus carpio).
A;Residues: Learned carpidation carpidation carpio Ciprinus carpio).
A;Residues: Learned carpidation c
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A; Rolecule type: DNA
A; Residues: 1-375 cNUD>
A; Residues: 1-375 cNUD>
A; Residues: 1-375 cNUD>
A; Cross-references: GB: 100691; NID: 9202653; PIDN: AAA40657.1; PID: 9202654
C; Comment: Vertebrate nonmuscle cells contain two highly conserved cytoskeletal actins, C; Genetics:
A; Introns: 41/3; 121/3; 268/1; 328/3
C; Superfamily: actin
C; Keywords: cell motility; cytoskeleton; methylated amino acid; microfilament; mitosis; F; 2-375/Product: actin beta #status predicted <a href="MAI">MAI">MAI</a>
F; 73/Modified site: 3'-methylhistidine (His) #status predicted
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C;Genetics:
C;Genetics:
C;Genetics:
C;Genetics:
C;Genetics:
C;Introns:
C;Introns:
C;Superfamily: actin
C;Superfamily:
C;Super
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C,Comment: Vertebrate nonmuscle cells contain two highly conserved cytoskeletal actins,
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                                          A; Experimental source: monocyte C; Comment: This protein is involved in a signal transduction that eventually leads C; Superfamily: actin
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C;Date: 13-Jun-1983 #sequence_revision 13-Jun-1983 #text_change 22-Jun-1999
C;Accession: A38571, A2999
R;Nudel, U; Zakut, R; Shani, M; Neuman, S; Levy, Z; Yaffe, D.
Nucleic, Acids Ree: 11, 175-1771, 1983
A;Title: The nucleotide sequence of the rat cytoplasmic beta-actin gene.
A;Reference number: A38571; MUID:83168920; PMID:6300777
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A, Residues: 1-61;84-112;147-190;196-209;215-253;335-358 <HA2>
                                                                                                                                                                                                                                                                                              Score 75; DB 2; I
Pred. No. 4.7e-06;
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Pred. No. 4.7e-06;
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100.0%; Pr
tive 0;
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Best Local Similarity 100.0%; P:
Matches 15; Conservative 0;
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Matches 15; Conservative
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C;Species: Acanthamoeba castellanii
C;Species: Acathamoeba castellanii
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C;Accession: A92886; A03004
C;Accession: A92886; A03004
J. Mol. Biol. 159, 1-18, 1982
A;Title: Actin genes and actin messenger RNA in Acanthamoeba castellanii. Nucleotide sequal A;Accession: A92886; MUID:83033627; PMID:6290670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1.375 <NEL>
A;Cross-references: UNIPROT:P02578; GB:V00002; GB:J01016; NID:g5565; PIDN:CAA23399.1; PIU
C;Comment: There are at least three actin genes in A. castellanii.
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Gaps
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C;Superfamily: actin
C;Keywords: methylated amino acid
F;73/Modified site: 3'-methylhistidine (His) #status predicted
Indels
ö
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Pred. No. 4.7e-06;
; Mismatches 0;
Mismatches
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Best Local Similarity 100.0%; Pi
Matches 15; Conservative 0;
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                                                                                             171 LPHAILRLDLAGRDL 185
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                                              1 LPHAILRLDLAGRDL
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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- protein search, using sw model OM protein

8, 2005, 09:58:56 ; Search time 57.8667 Seconds (without alignments) 132.739 Million cell updates/sec April Run on:

US-09-423-351C-7 75 1 LPHAILRLDLAGRDL 15 Perfect score: Sequence:

**BLOSUM62** Scoring table: 1612378 seqs, 512079187 residues Searched:

Gapop 10.0 , Gapext 0.5

1612378 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt 03:* Database

1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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Result No.	Score	Query Match	Length	DB	. di		
-	75	100.0	92	. ~	Q7M3Y5	O7m3y5 aplysia	sia cal
8	75	100.0	93	~	белоро		
٣	75	100.0	101	~	061569		ostertagia
4		100.0	104	~	Q11210		ca fasc
2	75	100.0	109	~	Q28916	Q28916 macaca	ca fusc
9	75	100.0	109	~	Q84LA4		
7	75	100.0	117	~	Q80012		
æ	75	100.0	117	N	Q80013		japoni
6		100.0	125	~	Q802E1		
10	75	100.0	125	7	Q802E2		pachycara b
	75	100.0	128	~	Q852Q7		marchantia
12	75	100.0	130	~	Q865G0		capra hircu
	75	100.0	132	~	Q91A84		stizostedio
14	75	100.0	133	~	Q9U4L7		ageniaspis
	75	100.0	133	~	Q9U4L8		ageniaspis
16	75	100.0	133	~	Q9U4L9	Q9u419 ageni	ageniaspis
17	75	100.0	133	~	Q9U4M0		ageniaspis
18	75	100.0	136	~	Q95V64	Q95v64 ixodes	ев всар
19	75	100.0	140	~	Q680U0		lepeophthei
20	75	100.0	142	~	Q9BGH4		oryctolagus
21	75	100.0	145	~	Q9LL42		trebouxia j
22	75	100.0	146	~	Q9Y191		u
23	75	100.0	147	~	004115		lla fru
24	75	100.0	150	~	Q68AX1	Q68ax1 cynops	ps pyrr
25	75	100.0	154	~	048669	-	cucumis sat
26	75	100.0	160	~	Q8T6A7		trichinella
27	75	100.0	162	~	Q6UBA0	-	onia my
28	75	100.0	165	~	Q8QFS7		scyliorhinu
29	75	100.0	167	~	Q76D36	Q76d36 costus	ns spec
30	75	100.0		~	Q76D37	COS	
31	75	100.0	169	7	Овѕркб	Q8spk6 sus s	scrofa

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O9nb01 metridium s O6b4v2 vitis vinif O7666 phyllostach O7xak3 asparagus o O8jh59 chelydra se Q86b3 botryllus s Q94y3 musa acumin Q6rx10 ficus caric Q86cv5 drosophila Q86tv8 drosophila Q94407 echinococcu Q94kc1 vitis vinif Q88114 asarina bar	
090NB01 06B4V2 076A6D6 077A6X3 08JHS9 0865B3 0865B3 086CV5 086CV5 096CV5 096CV5 094CC1 094KC1 098S31A	
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170 171 171 171 172 172 172 176 176 180 181	
27 27 27 27 27 27 27 27 27 27 27 27	
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ALIGNMENTS

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Aplysia california sea hare).
Bukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Apogastropoda; Heterobranchia; Buthyneura; Opisthobranchia; Anaspidea;
Aplysioidea; Aplysiidae; Aplysia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=88320566; PubMed=3413132;
Kennedy T.E., Gawinowicz M.A., Barzilai A., Kandel B.R., Sweatt J.D.;
"Sequencing of proteins from two-dimensional gels by using in situ
digestion and transfer of peptides to polyvinylidene difluoride
membranes: application to proteins associated with sensitization in
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PIR, A31409; A31409. Cactin cytoskeleton; IEA.

GO, GO:0015629; C:actin cytoskeleton; IEA.

GO, GO:0015629; C:actin cytoskeleton; IEA.

NON TER

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NON TER

92

SEQÜENCE 92 AA; 9513 MW; JG36BEFE381A701C CRC64;
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Pred. No. 3.8e-06;
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92 AA; 9513 MW; 3C36BEFE381A701C CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Actin (Fragment).
                                                                                                    Last sequence update)
Last annotation update)
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nes 15; Conservative
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Length 104;

Score 75; DB 2; L Pred. No. 4.4e-06;

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Hino A., Tokuyama Y., Kobayashi M., Yano M., Weir B., Takeda J., Bell G.I., Macdonald R.L.; Submitted (FBB-1995) to the EMBL/GenBank/DDBJ databases. EMBL; U20576; AAA62435.1; -- HSSP; Pl0983; 1D4X.
                                                                                                                                                                                                GO; GO:0015629; C:actin cytoskeleton; IEA.
GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
InterPro; IPRO022; Actin_like.
Pfam; PF00022; Actin, 1.
                                                                                                                                                                                                                                                                                                                                     104 AA; 11438 MW; 3610F3FEFA370C91 CRC64;
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100.0%;
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Best Local Similarity 100.0
Matches 15; Conservative
                                              SEQUENCE FROM N.A.
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NCBI_TaxID=9541;
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Q84LA4
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Bibli, AFOS2043; AAC06292.1; -. HSSP; P10983; 1D4X.
                                                                                                                                                                                                                                                                                                                                         Gaps
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Trichostrongyloidea, Haemonchidae, Ostertagiinae, Ostertagia.
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011210;
01-10V-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 24, Last annotation update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Beta-actin (Fragment).
Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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                         Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Orthopteroidea, Orthoptera, Caelifera, Acridomorpha,
Acridoidea, Romaleidae, Romalea.
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GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
InterPro: IPR004000; Actin_like.
Pfam; PF00022; Actin, 1.
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100.0%; Pred. No. 3.8e-06;
tive 0; Mismatches 0; Indels
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100.0%; Pred. No. 4.2e-06;
tive 0; Mismatches 0; Indels
                                                                                                                                                       Fei H., Martin T., Jaskowiack K., Hatle J., Borst D.W.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases
EMBL; AY331667; AAQ24502.1; -.
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101 AA; 11499 MW; 7AF3A21892AD0D75 CRC64;
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Last sequence·update)
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      Romalea microptera (Lubber grasshopper)
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                                                                                        NCBI_TaxID=7007;
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MEDILINE=96071113; PubMed=7577717; DOI=10.1016/0960-0760(95)00157-U;
Yamada-Mouri N., Hirata S., Hayashi M., Kato J.;
Yamada-Mouri N., Hirata S., Hayashi M., Kato J.;
"Analysis of the expression and the first exon of aromatase mRNA in monkey brain.";
J. Seroid Biochem. Mol. Biol. 55:17-23(1995).
HSSP; P10983; 1D4X.
                                                                                                                                                                                                                                                                                                                                                                     Macaca fuscata (Japanese macaque).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
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GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
InterPro; IPR004000; Actin_like.
Pfam; PF00022; Actin; 1.
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Last annotation update)
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01-NAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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01-JUN-2003 (TrEMBLrel. 24,
01-MAR-2004 (TrEMBLrel. 26,
Actin (Fragment).
                                                                                       42 LPHAILRLDLAGRDL 56
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Best Local Similarity 100.
Matches 15; Conservative
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                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cercopithecinae, Macaca
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arundinacea (Tall fescue) (Schedonorus arundinaceus)

SEQUENCE

Matches

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Zoarcoidei;
                                                                                                                                    Hyla japonica (Japanese tree frog).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ducassen M., Sokolov E., Poertner H.-O.;
Submitted (JAN-2003) to the EMEL/GenBank/DDBJ databases.
Submitted (JAN-2003) to the EMEL/GenBank/DDBJ databases.
-!- FUNCTION: Actins are highly conserved proteins that are involved in various types of cell motility and are ubiquitously expressed in all eukaryotic cells (By similarity).
-!- SIMILARITY: Belongs to the actin family.
EMBL: AV27658; AAO72722.1; -.
HSSP; PG0712; 1HUJ.
GO; GO:0015629; C:actin cytoskeleton; IEA.
GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
                                                                                                                                                                                                                                                      GO; GO:0015629; C:actin cytoskeleton; IEA.
GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
InterPro; IPR004000; Actin_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 75; DB 2; Length 117; 100.0%; Pred. No. 5e-06; Live 0; Mismatches 0; Indels
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117 AA; 13291 MW; 64C6BAC4F84184CF CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                          Last sequence update)
Last annotation update)
                              117 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00190; ACTIN.
PROSITE; PS01132; ACTINS_ACT_LIKE; 1.
                                                             Created)
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                              PRT;
                                           08-0013;
01-JUN-2003 (TrEMBLrel. 24,
01-JUN-2003 (TrEMBLrel. 24,
01-MAR-2004 (TrEMBLrel. 26,
Beta-actin 1 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92 LPHAILRLDLAGRDL 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 LPHAILRLDLAGRDL 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                PRELIMINARY;
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NCBI_TaxID=48416;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Structural protein.
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Matches 15; Conserv
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                                                                                                                                                                                              NCBI_TaxID=109175;
                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                 TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=ACT-B;
                                                                                                                          Name=ACTB1;
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Q802E1;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Amphibia, Batrachia, Anura, Neobatrachia, Hyloidea, Hylidae, Hylinae,
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Poeae; Schedonorus.
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                                                                                                                                                                      GO; GO:0015629; C:actin cytoskeleton; IEA.
GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
InterPro; IPRO002; Actin_like.
Pfam; PF00022; Actin_1.
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Pred. No. 5e-06;
                                                                                                                                                                                                                                                                                                Length 109;
                                                                                                        Johnson L.J., Johnson R.D., Schardl C.L., Panaccione D.G., Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases. EMBL, AX194227, AAO40042.2; -- HSSP, P02577; INML.
                                                                                                                                                                                                                                                                                                                            0; Indels
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109 AA; 12177 MW; 10780BBA52F6E8EA CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Beta-actin 2 (Fragment).
                                                                                                                                                                                                                                                                                               Score 75; DB 2; 1
Pred. No. 4.6e-06;
                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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Best Local Similarity 100.0
Matches 15, Conservative
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Best Local Similarity
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                                                                           FROM N.A.
                                                                                           TISSUE=Pseudostem
                                                 NCBI_TaxID=4606;
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Gaps

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Marchantia polymorpha (Liverwort).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Marchantiophyta,
Marchantiopsida, Marchantiidae, Marchantiales, Marchantiineae;
Marchantiaceae, Marchantii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sharmila C., Reddy P.G.;
Sharmila C., Reddy P.G.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Actions are highly conserved proteins that are involved
-!- FUNCTION: Actions are highly conserved proteins that are involved
-!- FUNCTION: Actions are highly conserved proteins that are involved
-!- SIMILARITY: Belongs to the actin family.
EMBL; AF481159; AAO49278.1; --
EMBL; AF481159; AAO49278.1; --
EMSL; P60712; HLU.
GO; GO:0015629; C:actin cytoskeleton; IEA.
GO; GO:0005200; F:structural constituent of cytoskeleton; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
Caprinae, Capra.
                                                                                                                                                                                                                  GO; GO:0015629; C:actin cytoskeleton; IEA.
GO; GO:0002500; R:structural constituent of cytoskeleton; IEA.
InterPro; IPR004000; Actin_like.
Pfam; PF00022; Actin; 1.
NON TER 12
NON TER 128
SEQUENCE 128 AA; 14527 MW; 53A33892EB2E608C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 75; DB 2; Length 130; 100.0%; Pred. No. 5.6e-06; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                             Score 75; DB 2; Length 128; Pred. No. 5.5e-06;
                                                                                                                                  Ahida Y., Fujii Y., Hirata T.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AB100427; BAC55601.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   130 130 130 130 MW; E817FD365B33EA3F CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Beta-actin (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 130 AA.
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PROSITE; PS01132; ACTINS_ACT_LIKE; 1.
Structural protein.
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Best Local Similarity 100.0
Matches 15; Conservative
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Best Local Similarity 100.
Matches 15; Conservative
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                                                                                                     [1]
SEQUENCE FROM N.A.
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                                                                                 NCBI_TaxID=3197;
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Actinopterygii, Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Zoarcoidei;
Zoarcidae; Pachycara.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lucassen M., Sokolov E., Poertner H.-O.;
Lucassen M., Sokolov E., Poertner H.-O.;
Lucassen M., Sokolov E., Poertner H.-O.;
Submitted (JAN-2003) to the EMBL/Genbank/DDBJ databases.
-I- FUNCTION: Actins are highly conserved proteins that are involved in various types of cell motility and are ubiquitously expressed in all eukaryoric cells (By similarity).
-I- SIMILARITY: Belongs to the actin family.
BMBL; AX227657; AAO72721.1; --
BMBL; AX227657; AAO72721.1; --
GO; GO:0015629; C:actin cytoskeleton; IEA.
GO; GO:0015629; C:actin cytoskeleton; IEA.
InterPro; IRP004000; Actin_like.
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                                                                                                                                                                               Length 125;
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100.0%; Pred. No. 5.4e-06;
tive 0; Mismatches 0; Indels
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100.0%; Pred. No. 5.4e-06;
tive 0; Mismatches 0; Indels
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                                                                                                                                        7B33EA4CF5EA88B0 CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JAM-2004 (TrEMBLrel. 26, Last annotation update)
Beta actin (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                   125 AA
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PROSITE; PS01132; ACTINS_ACT_LIKE; 1.
                                                           PROSITE; PS01132; ACTINS_ACT_LIKE; 1
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InterPro; IPR004000; Actin_like
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125 AA; 14100 MW;
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125 AA; 14100 MW;
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                                                                                                                                                                                                                                                          1 LPHAILRLDLAGRDL 15
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                                                                                                                                                                                               Best Local Similarity 100.
Matches 15; Conservative
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Best Local Similarity 100.
Matches 15; Conservative
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                  Pfam; PF00022; Actin; 1
PRINTS; PR00190; ACTIN
                                                                               Structural protein.
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Q852Q7;
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RESULT 10
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AC 080288
AC 08028
DJ 01-JU
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Gaps

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0; Indels

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RESULT 13 Q9IA84

Last sequence update)
Last annotation update)

Actin (Fragment) Name=MpACT1;

RESULT 11
Q852Q7
ID Q852Q
AC Q852Q
DT 01-JU
DT 01-JU
DT 01-MA
DE Actin
GN Name=

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GO:0005200; F:structural constituent of cytoskeleton; IEA
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Hoy M.A., Jeyaprakash A., Morakote R., Lo P.K.C., Nguyen R.;
"Genomic analyses of two populations of Ageniaspis citricola
"Genomic analyses of two populations of Ageniaspis citricola
(Hymenoptera: Encyttidae) suggest that a cryptic species may exist.";
Biol. Control 17:1-10(2000)
-!- FUNCTION: Actins are highly conserved proteins that are involved
in various types of cell motility and are ubiquitously expressed
in all eukaryotic cells (By similarity).
-!- SIMILARITY: Balongs to the actin family.
EMBL, AF164631; AAF2279:1;
-- HSSP; P10983; 104X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cyclin).";
Virology 280:31-40(2001).
Virology 280:31-40(2001).
-- PUNCTION: Actins are highly conserved proteins that are involved in various types of cell motility and are ubiquitously expressed in all enkaryotic cells (By similarity).
-- SIMILARITY: Belongs to the actin family.
EMBL; AP21944; AAP31439.1; --
HSSP; P60712; 1HJU.
GO; GO:0015629; C:actin cytoskeleton; IEA.
GO; GO:005200; F:structural constituent of cytoskeleton; IEA.
Interpro; IRP004000; Actin_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidei;
Percidae; Stizostedion.
                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21109119; PubMed=11162816; DOI=10.1006/viro.2000.0731;
Rovnak J., Casey J.W., Quackenbush S.L.;
"Intracellular targeting of walleye dermal sarcoma virus Orf A (rv-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ô
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Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Hymenoptera, Apocrita, Chalcidoidea,
Broyttidae, Encyttinae, Ageniaspis.
NCBI_TaxID=105762;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 75; DB 2; Length 13:
100.0%; Pred. No. 5.7e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      132 AA; 14886 MW; D78E91FB00A65E8E CRC64;
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01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Actin 2 (Fragment)
                                                                             Last sequence update)
Last annotation update)
132 AA
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                                                      Created)
PRT;
                                             (TrEMBLrel. 15, C
(TrEMBLrel. 15, I
(TrEMBLrel. 24, I
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PRELIMINARY;
                                                                                                                                Beta actin (Fragment). Stizostedion vitreum.
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                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Dermal sarcoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Structural protein.
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les 15; Conserv
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                                                                                                                                                                                                                                                                                                NCBI_TaxID=57868;
                                                   01-OCT-2000
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Neoptera; Endopterygota; Hymenoptera; Apocrita; Chalcidoidea;
Encyrtidae; Encyrtinae; Ageniaspis.
NCBI_TaxID=105762;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 75; DB 2; Length 133; 100.0%; Pred. No. 5.8e-06; ive 0; Mismatches 0; Indels
                                                                                                                                                  Score 75; DB 2; Length 133;
Pred. No. 5.8e-06;
                                                                                                                                                                                   0; Indels
                                                                                                  133 AA; 14955 MW; 27DFC1FF30D4984F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                     133 AA.
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PROSITE; PS01132; ACTINS_ACT_LIKE; 1.
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InterPro; IPR004000, Actin_like.
PERM; PF00022, Actin, I.
PRINTS; PR00190; ACTIN.
PROSITE; PS01132; ACTINS_ACT_LIKE;
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Best Local Similarity 100.
Matches 15; Conservative
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                                                               Structural protein.
NON TER 133 13
SEQUENCE 133 AA; 1
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